







Best Local Similarity 87.9%; Pred. No. 0; Matches 1803; Conservative 0; Mismatches 9; Indels 240; Gaps 3;			
QY	2180	TCTCTCTCAGGTAGAGAAAGAGGCTGAAGCTAAAGCTGTAGCTATGGGTCAAGCCCTAGA	2239
Db	441	TTTCTCAGGTAGAGAAAGAGGCTGAAGCTAAAGCTGTAGCTATGGGTCAAGCCCTAGA	500
QY	2240	CATAGCTATTCTCTCCACCGCTTAAGCGTAAACCAAACTCTTATCTCGAAAGAC	2299
Db	501	CATAGCTATTCTCTCCACCGCTTAAGCGTAAACCAAACTCTTATCTCGAAAGAC	560
QY	2300	GGGAAGTCGAAGCATCTTATGTCAAAACCGGTGTGAATGATGAAGAGTCCCTTGG	2359
Db	561	GGGAAGTCGAAGCATCTTATGTCAAAACCGGTGTGAATGATGAAGAGTCCCTTGG	620
QY	2360	ATCAGAAAAGTGTCCCATCTCTGAGGTGATTTTCATGGTCTATATGGCATCTTTTTCAGT	2419
Db	621	ATCAGAAAAGTGTCCCATCTCTGAGGTGATTTTCATGGTCTATATGGCATCTTTTTCAGT	2419
QY	2420	GTGTACATTTGCTCTCATGTTTAAATACAGATTGTGTGCTTCGTTTATATAGTCCCAA	2479
Db	644	-----AGATGGCCAA	653
QY	2480	TGAAGTCGACAACTAAAGCCTGAAGAGAACTCTGCAGGAGCAACTGTTTACA	2539
Db	654	TGAAGTCGACAACTAAAGCCTGAAGAGAACTCTGCAGGAGCAACTGTTTACA	713
QY	2540	TTGTTTCACTCATAGTATCTCTCTGCTGCTATCTCCATGAATAAAAGTTGTATAGAC	2599
Db	714	TTGTTTCACTCATAGTATCTCTCTGCTGCTATCTCCATGAATAAAAGTTGTATAGAC	773
QY	2600	ATCAAAACGCAAGCATCTTTCGGGAGTCTTTCGGCTTACGGGAAGGTTAAATAAATCT	2659
Db	774	ATCAAAACGCAAGCATCTTTCGGGAGTCTTTCGGCTTACGGGAAG	817
QY	2660	TTCTATTGCTATTGAGGTTTTAAGACGATTAGTACTTTTCATGAATCAAAACCGTGGG	2719
Db	818	-----	817
QY	2720	GAATAACAGGGAAGTCAGATAACAGGGTAAGAAAGGAGTCAAACTCAGATTTGAATCA	2779
Db	818	-----AGGGAAGTCAGATAACAGGGTAAGAAAGGAGTCAAACTCAGATTTGAATCA	870
QY	2780	AAATCTCTGGAAGCGTAAATGAGCAAGCACTCTGAGCTTATCCGATGCATATCCCTGTG	2839
Db	871	AAATCTCTGGAAGCGTAAATGAGCAAGCACTCTGAGCTTATCCGATGCATATCCCTGTG	930
QY	2840	CTAGTGCCATTGGGGAGCTCAATAACAAGTTCTCTATCACATCTCTCTTCCAGAGCCAGAT	2899
Db	931	CTAGTGCCATTGGGGAGCTCAATAACAAGTTCTCTATCACATCTCTCTTCCAGAGCCAGAT	990
QY	2900	AGTCATCCCCACACAGTTGCAGGAGATTATCAGTCTGTTTCTTAATCATATAATGTCAACC	2959
Db	991	AGTCATCCCCACACAGTTGCAGGAGATTATCAGTCTGTTTCTTAATCATATAATGTCAACC	1050
QY	2960	CTTTTACAAACACCGGCTTTTATCTCCGCAACTTTCCGCTCATCATATTTTGGCTCCC	3019
Db	1051	CTTTTACAAACACCGGCTTTTATCTCCGCAACTTTCCGCTCATCATATTTTGGCTCCC	1110
QY	3020	GATTCTAGTGTGGCTCACCTGTTCCAGGGAACCTCACCTCCGAATCTCGCTGCGCATGGCC	3079
Db	1111	GATTCTAGTGTGGCTCACCTGTTCCAGGGAACCTCACCTCCGAATCTCGCTGCGCATGGCC	1170
QY	3080	GCAGCCACTGTTCAGCTGTAGTGTGGTGGCTGCCAATGGAATTAATACCTTTATGT	3139
Db	1171	GCAGCCACTGTTCAGCTGTAGTGTGGTGGCTGCCAATGGAATTAATACCTTTATGT	1230
QY	3140	GCTCCTCTTACCTCAGGTTGTTTCACTAGTATCTCTCATCTCTTTTGGACCATCATGT	3199
Db	1231	GCTCCTCTTACCTCAGGTTGTTTCACTAGTATCTCTCATCTCTTTTGGACCATCATGT	1290
QY	3200	GATGTAGAGTACACAAAGACGACATTTTCAACAATGTTCTGTGACAGCCGAGACAA	3259
Db		-----	

Db	1291	GATGTAGAGTACACAAAGCAAGCACTTTTCAACATGTTCTGTGACAGAGCCGAGACAA	1350
QY	3260	GAACACTCCGAGGATCAAAAGCTCGATCTTCACTGGACTCAGAGATGTTTCAAAATAG	3319
Db	1351	GAACACTCCGAGGATCAAAAGCTCGATCTTCACTGGACTCAGAGATGTTTCAAAATAG	1410
QY	3320	AGTAAACAGTGTTCATGAGCAGCTTCTGCAACACCTCGAGAGTATGCAAAAGGTTCA	3379
Db	1411	AGTAAACAGTGTTCATGAGCAGCTTCTGCAACACCTCGAGAGTATGCAAAAGGTTCA	1470
QY	3380	GATGAGCAGAGACAGAAAAAAGTTGACCGGTCTCTGTGTGGCTCAAAACACTCCGTGC	3439
Db	1471	GATGAGCAGAGACAGAAAAAAGTTGACCGGTCTCTGTGTGGCTCAAAACACTCCGTGC	1530
QY	3440	AGTAGTGATGATGTTGAGCGGATCATCAGAAAGCGAGAGTGGACCAATGGTGAG	3499
Db	1531	AGTAGTGATGATGTTGAGCGGATCATCAGAAAGCGAGAGTGGACCAATGGTGAG	1590
QY	3500	GTGAAAGAAACGAATGAAGACACTTAATAAACCTTCAAGCTTCAAGTCCAAATGCAGCCGC	3559
Db	1591	GTGAAAGAAACGAATGAAGACACTTAATAAACCTTCAAGCTTCAAGTCCAAATGCAGCCGC	1650
QY	3560	AGTAGAATCAGCTCCAATATTAACCGATCCATGGAAAGTCTGTCTGTGACGAGGTACTTACT	3619
Db	1651	AGTAGAATCAGCTCCAATATTAACCGATCCATGGAAAGTCTGTCTGTGACGAGGTACTTACT	1700
QY	3620	TGGACTAAAGATCAACTTCTTTTCAAAATCATTTTCTCATATAAATATTTGTACATTC	3679
Db	1701	-----	1700
QY	3680	GGGTGGAATTCGCTTCCAAAGCTCTCTTCCAGAGAGGTATTTGCCGCAAAAGTTTACATA	3739
Db	1701	GGGTGGAATTCGCTTCCAAAGCTCTCTTCCAGAGAGGTATTTGCCGCAAAAGTTTACATA	1760
QY	3740	TCGAGAGAAACACAGAGAGGAGAAACAACAACAAGAAATATCCAATGGCACT	3799
Db	1761	TCGAGAGAAACACAGAGAGGAGAAACAACAACAAGAAATATCCAATGGCACT	1820
QY	3800	TGATCTTAATCTCACAGCTCAGTTTAAACACAGTTTGAATGATCAAGAGGAGAGAAACAC	3859
Db	1821	TGATCTTAATCTCACAGCTCAGTTTAAACACAGTTTGAATGATCAAGAGGAGAGAAACAC	1880
QY	3860	AGGATTTCTTGGAAATCGGATTAGATGCTTCAAAAGCTAATAGTAGAGGAGAGAAACAGTTT	3919
Db	1881	AGGATTTCTTGGAAATCGGATTAGATGCTTCAAAAGCTAATAGTAGAGGAGAGAAACAGTTT	1940
QY	3920	TAAACCATACAAAAGATGTTCCATGGAAAGCAAAAGAAAGTAGAATCTCTCAACAATCC	3979
Db	1941	TAAACCATACAAAAGATGTTCCATGGAAAGCAAAAGAAAGTAGAATCTCTCAACAATCC	2000
QY	3980	TATCATTTTCATCTGGAAACAGAAAGATCCCAACCGATCGGTTGGAAACCTCAGCTTCCAC	4039
Db	2001	TATCATTTTCATCTGGAAACAGAAAGATCCCAACCGATCGGTTGGAAACCTCAGCTTCCAC	2060
QY	4040	ATGAGACTCTATTTTTCATCTGATCTGTTTGTGTTGTTGTTTAAAGTTTCAAGACCA	4099
Db	2061	ATGAGACTCTATTTTTCATCTGATCTGTTTGTGTTGTTGTTTAAAGTTTCAAGACCA	2120
QY	4100	CTGCTACATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	4159
Db	2121	CTGCTACATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	2180
QY	4160	TGTAACATTTTCTGCTCTGTTTATTTTCAACAAATCATATAATCTTTTAACTTTTCTTTTCTTTT	4219
Db	2181	TGTAACATTTTCTGCTCTGTTTATTTTCAACAAATCATATAATCTTTTAACTTTTCTTTTCTTTT	4240
QY	4220	ACCTGGAAAGAA 4231	
Db	2241	AAAAAAAAAAAAA 2252	

RESULT 3  
US-09-202-712-6



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; Sequence 6, Application US/09202712
; Patent No. 6265637
; GENERAL INFORMATION:
; APPLICANT: Coupland, George M
; APPLICANT: Schaffer, Robert J
; TITLE OF INVENTION: Genetic control of flowering
; FILE REFERENCE: 620-55
; CURRENT APPLICATION NUMBER: US/09/202,712
; CURRENT FILING DATE: 1999-01-11
; EARLIER APPLICATION NUMBER: PCT/GB97/01676
; EARLIER FILING DATE: 1997-06-23
; EARLIER APPLICATION NUMBER: GB 9613132.1
; EARLIER FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutant
US-09-202-712-6

Query Match
Best Local Similarity 2.1%; Score 90.4; DB 3; Length 666;
Matches 193; Conservative 1; Mismatches 77; Indels 37; Gaps 2;

QY 1444 TATAGACTCGGAAGCCATATACGATAACAAAGCAACGTTGAAAGTGGACTGAGGAAGAAC 1503
DB 284 TTATAGCAAGAAAGCCATATACATATACAAACAGCAGGAGCGATGGACTGAGGATGAGC 343
QY 1504 ATATAGATTTCATTGAGGCTTTGAGGCTTTATGTTAGAGCATGGCAGAGGATTTGAAGTT 1563
DB 344 ATGAGAGGTTTCTAGAGGCTTTGAGGCTTTATGGAAGAGCTTTGGCAAGCAATTGAAGTTC 403
QY 1564 G-----ATTTTATTTCCCTTATATCTCTATTTTGTGTTGAG 1606
DB 404 GRAAGGTTTATCTTTTGAATGTTAGTTGAACTCTTTGAGATTTTATATCTCTTTGTTT 463
QY 1607 AGTTTGTCTTCA-----AACTGATTTCCTTTTTCATTGGAC 1646
DB 464 AGGAGTGCTTTATCTCTCTTTGTTGGAGATTCTTCTTTTCATTGTTGTC 523
QY 1647 AGACATGTAGCAACAAAGCTGCTGTCAGATAGAGTCAAGTCAAGTCAAGATTTTCTC 1706
DB 524 AGACATATTGGGACAAAGACTGCTGTTGAGATCAGATCAGAAAGTCAAGCAAAAGTTCTTCA 583
QY 1707 CAAGGTAA 1714
DB 584 AAAGGTAA 591

RESULT 4
US-09-202-712-1
; Sequence 1, Application US/09202712
; Patent No. 6265637
; GENERAL INFORMATION:
; APPLICANT: Coupland, George M
; APPLICANT: Schaffer, Robert J
; TITLE OF INVENTION: Genetic control of flowering
; FILE REFERENCE: 620-55
; CURRENT APPLICATION NUMBER: US/09/202,712
; CURRENT FILING DATE: 1999-01-11
; EARLIER APPLICATION NUMBER: PCT/GB97/01676
; EARLIER FILING DATE: 1997-06-23
; EARLIER APPLICATION NUMBER: GB 9613132.1
; EARLIER FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2526
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana

; FEATURE:
; NAME/KEY: CDS
; LOCATION: (338)..(2275)
US-09-202-712-1

Query Match
Best Local Similarity 1.9%; Score 83.2; DB 3; Length 2526;
Matches 233; Conservative 0; Mismatches 213; Indels 12; Gaps 1;

QY 2847 CATTGGGAGCTCAATACAAAGTTCTTATCATCATCTCTCTCAGAGCCAGATAGTATC 2906
DB 1137 CATCTGCTACTACTACAGCTTCTCATCAAGCGCTTTCCAGCTTGTTCATTACAGGATGAT 1196
QY 2907 CCCACACAGTTGCAGGAGATTATCAGTCGTTTCTTAATCATATAATGTCAACCTTTTAC 2966
DB 1197 ACCGTTTCGTTCTCCAGATATCATCTACTTCTTCAATCTTATATGTCAACTCTCTAC 1256
QY 2967 AAACACCGGCTCTTTATATCTGCGCAACTTTCCGCTCATCTTTTGGCTTCCCG----- 3020
DB 1257 AGAATCCTGCAGCTCATGCTGCAGCTACATTCGCTCGCTTGGCTTATGCGAGTG 1316
QY 3021 -----ATTCTAGTGGTGGCTCACCTGTTCCAGGGAACCTCACCTCCGAATCTGGCTGCCA 3074
DB 1317 TCGGGAATTCGTTGATTTCATCAACCCCAATGAGCTCTTCTCTCAAGTATAAATGCA 1376
QY 3075 TGGCCGAGCCACTGTTGCAGCTGCTAGTGTGTTGGGCTGCCAATGATTATTACCTT 3134
DB 1377 TTGCGCTGCTACAGTAGCTGCTGCAACTGCTTTGGTGGCTTCTCATGACTTCTTCTCTG 1436
QY 3135 TATGTCCTCTTATGTTAGTTCAGTGTTTCACTAGTATCTCTCCATCTACTTTTGGACCAT 3194
DB 1437 TATGCTCCAGCTCCAATAACATGTGTTCCATTCTCAACTGTGTCAGTTTCCAACCTCCAG 1496
QY 3195 CATGTGATGTAGAGTACACAAAGCAAGCACTTTTACAACATGTTCTGTGAGAGCCGAG 3254
DB 1497 CAATCACTGAAATGATACCGTTGAAATACTCAACCGTTTGAGAAACAAACACAGCTC 1556
QY 3255 AGCAAGAACACTCCAGGATCAAAAGGCTCGATCTTCA 3292
DB 1557 TGCAGATCAAACTTGGCTTGAATCTCCAGCTTCA 1594

RESULT 5
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232.463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935.313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZ9pt-Fls
; US-08-232-463-14

Query Match 1.2%; Score 54.2; DB 1; Length 7218;
Best Local Similarity 3.3%; Pred. No. 0.0014;
Matches 11; Conservative 195; Mismatches 123; Indels 0; Gaps 0;

QY 3711 AGAGAGGTATGCGCAAGTTTACATATCGAGAAGAACACAGAGAGGAGAACAA 3770
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1380 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1321
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 3771 CAACAGAACAAGATATCAATGCGCACTTGATCTTAACCTTCACACCTCAGTTAACACCA 3830
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1320 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1261
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 3831 GTTGATGATCAAGAGAGAGAGAAACACAGGATTTCTTGGAATCGGATTAGATGCTTCA 3890
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1260 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1201
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 3891 AAGCTAATCAGTAGAGAGAACAGGTTTAAACCATACAAAGATGTTCCATGGAAGCC 3950
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1200 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1141
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 3951 AAAGAAAGTAGAATCTCAACAAATCTATCATTCATGTGGAACAGAAAGATCCCAA 4010
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1140 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1081
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 4011 CGGATCGGTGGAAGTCAAGCTCCAC 4039
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1080 RRRRRRRRRRRRRATCGCAAGCTCCCTC 1052
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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## RESULT 6

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US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZ9pt-Fls
; US-08-232-463-14

Query Match 1.2%; Score 51.4; DB 1; Length 7218;
Best Local Similarity 2.6%; Pred. No. 0.0068;
Matches 7; Conservative 168; Mismatches 94; Indels 0; Gaps 0;

QY 1006 GTGGCTGAGATTTCCTCATTCCTGGTCTCTTTCTTTGTTTCATGATCAA 1065
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1056 GAGCTTGCATYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYV 1115
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1066 AAGCAATCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1125
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1116 YVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYV 1175
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1126 ATCTGGAATTAATAATGGAATCTTATCGAATCAAGCTGATTTCGTTCTTCA 1185
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1176 YVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYV 1235
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1186 TCATCTCTCTAAAGGTACTTAAGATGATTATGTCATGGTCTTTCTTATGTTGATG 1245
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1236 YVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYV 1295
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1246 AATACTTGACTTGATTGTTTGTGTTT 1274
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1296 YVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYV 1324
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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## RESULT 7

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US-08-487-826B-13/c
; Sequence 13, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobb Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.2.25
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/487,826B
;
; FILING DATE: 10-SEP-1993
;
; CLASSIFICATION: 435
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Israelsen, Ned
;
; REGISTRATION NUMBER: 29,655
;
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: (619) 235-8550
;
; TELEFAX: (619) 235-0176
;
; INFORMATION FOR SEQ ID NO: 13:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 19124 base pairs
;
; TYPE: nucleic acid
;
; STRANDEDNESS: single
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: cDNA
;
; HYPOTHETICAL: NO
;
; ANTI-SENSE: NO
;
; US-08-487-826B-13

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Query Match	1.2%	Score 51.2;	DB 2;	Length 19124;
Best Local Similarity	46.7%;	Pred. No. 0.012;		
Matches 199;	Conservative 0;	Mismatches 223;	Indels 3;	Gaps 1;
Qy	965	AAATAAATAAAATFAAAAAAGTTTGAGCTTAAAGAGATAATTATACGTGCTGAGATTTCTCCCAT	1024	
Db	16004	ATATATATATATATATGATGATATATGTCGATGTAATTAATTTTATTTTATTTTATTTTAT	15945	
Qy	1025	TTCGGTAGCTTCGGTCTCTTTTGTGTTTCATTGATCAAAAGCAAAATCACTTCTCTT	1084	
Db	15944	TTAATFAAAATTTTTTATTTTATTTTATTTTCATTAATAATTTTTTAAATTTTTTATTTTATTTA	15885	
Qy	1085	CTTCTTCTCTCGATTTCTTACTGTTTCTCTATCCAACGAATCTGGAATCTAAAAATCGA	1144	
Db	15884	ATTAAATTTTTTATTTATTTATTTTATTTTATTTTAAATTTTATTTTATTTATTTATTTT	15825	
Qy	1145	ATCTTTATCGAATCCAAGCTGATTTTGTGTTCTTTCATTGAATCATCTCTCTAAAGGTACT	1204	
Db	15824	TTTTTATTTAAAT--AAATTTTTTTTATTTTATGATATATTTTTTTTTTAAACATTTT	15768	
Qy	1205	TAGATTTGATTTATGTCATGCTTCTTCTATTTGTTGATGAAATCACTGACTGATGT	1264	
Db	15767	TTAATTTTTTTTTTATTTAATGATATAATTTTTTATTTTAAATATATTTTTTCTTTTTTTT	15708	
Qy	1265	TTTTGTTTTGTGGATTAGTGGAAATTTGTGTAAGAGAAAGATCTGAAGTTGCTAGAGGAG	1324	
Db	15707	TGTGTTTTATGATATATATTTTTTTTTTTTTTTTTTAAATGTTTTTTTTTCTCTTTGTTTTT	15648	
Qy	1325	CTTAGTGATGGACACAAATTCCTCTGGAGAGATCTGTTATTATAGGTAAATTAACATAA	1384	
Db	15647	ATTTTTTTTATATCAATTTTTTTTTTTTTTATATAAAAAATTTTTTTTAAATTTTTTTTGATAAT	15588	
Qy	1385	TTTTT 1388		
Db	15587	CTTT 15584		

RESULT 8  
US-09-202-712-19  
; Sequence 19, Application US/09202712  
; Patent No. 6265637  
; GENERAL INFORMATION:  
; APPLICANT: Coupland, George M  
; APPLICANT: Schaffer, Robert J  
; TITLE OF INVENTION: Genetic control of flowering  
; FILE REFERENCE: 620-55  
; CURRENT APPLICATION NUMBER: US/09/202,712  
; CURRENT FILING DATE: 1999-01-11  
; EARLIER APPLICATION NUMBER: PCT/GB97/01676  
; EARLIER FILING DATE: 1997-06-23

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; EARLIER APPLICATION NUMBER: GB 9613132.1
; EARLIER FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 19
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Nucleotide
; OTHER INFORMATION: sequence of EST 16213T7, Accession no. R30439
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (37, 204, 275, 335, 347, 353, 363, 367)
; OTHER INFORMATION: n is a, g, c, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (377, 384, 392, 393, 419, 428, 429, 436, 439)
; OTHER INFORMATION: n is a, g, c, or t
US-09-202-712-19

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	Query Match	1.1%	Score 46.2	DB 3	Length 447	
	Best Local Similarity	62.1%	Pred. No. 0.04			
	Matches	72	Conservative	0	Mismatches 44	Indels 0
						Gaps 0
Qy	1453	GGAAGCCATATACGATTAACAAGCAACGCGTAAAGGTGGACTGAGGAGAAACATAATAGAT	1512			
Db	150	GGAAAGCTTACACAAATCACCACGCTAGAGAGAGTTGGACTGAAGGAGAACACGCNCAAGT	209			
Qy	1513	TCATTGAAGCTTTGAGGCTTTATGGTAGACCTGGCAGAAAGATGTGAAGGTGGATTT	1568			
Db	.210	TTCTGGAAGCTCTTCAATTGTTTGGTCGTGACTTGGAAAAGAGATAGAAGATTTTTTTT	265			

## RESULT 9

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US-09-523-999A-1/c
; Sequence 1, Application US/09523899A
; Patent No. 6544789
; GENERAL INFORMATION:
; APPLICANT: Raskin, Ilva
; APPLICANT: Haran, Shoshan
; TITLE OF INVENTION: Phosphorus-Cont
; FILE REFERENCE: 29155/35950
; CURRENT APPLICATION NUMBER: US/09/5
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 09/015,601
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1274
; TYPE: DNA
; ORGANISM: A. thaliana
; FEATURE:
; OTHER INFORMATION: A. thaliana acia
US-09-523-999A-1

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	Query Match	1.0%;	Score 45.6;	DB 4;	Length 1274;
	Best Local Similarity	45.3%;	Pred. No. 0.09;		
	Matches 243;	Conservative 0;	Mismatches 289;	Indels 4;	Gaps 2;
QY	980	AAAGTTTGAGGTTAAAGATAATTATAGTCGGCTGAGATTTCCTCCATTTCGGTAGCTCTCTGG	1039		
Db	851	AAAGTTTCTCGAAGAGAAACATCTCTCCTTCTCTCATATTTTCTCTCTCTCTCTCA	792		
QY	1040	TCCTTTCTCTTTGTTTCATTGATCAAAAGCAAAATCACTTCTCTCTCTCTCTCTCTCGAT	1099		
Db	791	TAATTTTTTTTTTGGTGATCTCTCATTTGAGATCTTCCAAAGAAAATGCTCTAACTATCT	732		
QY	1100	TTCTTACTGTTTTCTTATCCACGAAATCTCGAAATTAAAAATGGAAATCTTTATCGAATCC	1159		
Db	731	TTTTTTTTTTTTTAAATATCGATTAATAAGTGTTGTAGGAAA--CAATTGATAGTGTGTCT	674		

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QY 1160 AAGCTGATTTGTTCTTTCAATGAATCATCTCTCTAAAGGTACTTAAGATTGATTTATT 1219
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Db 673 TTCAATTTTCTTACAGATTTTAAACACAGATTTGAATGTA--AAATGAAGCTTTTTT 616
      |||||
QY 1220 GTCATGGCTTTCTTATTTGTTGATGAATAACTTGGACTTGAATTTGTTTGTGGA 1279
      |||||
Db 615 AAAAATATATTTTCAATACCTTTTGTGTTAGGAAGGGTTATTCGTTTATAGATTTATAAT 556
      |||||
QY 1280 TTAGTGGATTTTGTAAAGAGAGAGACTGAAGTTGTTAGAGGAGCTTAGTGATGAGAC 1339
      |||||
Db 555 GAATTTGAAATCCGACAAAATTCATTTGTAATTTAAATTTAAATTTAAATTTAAAT 496
      |||||
QY 1340 AAATTCCTCGGAGAGATCTGGTTATTAAGGTAAATTAATACTAAATTTTAGGGGGAAGAT 1399
      |||||
Db 495 AATATCATGTTGTTATGATTCATGATTTTATAAATACTAGTTAAATCCTTTGTATTGCG 436
      |||||
QY 1400 GATTGTTTGGTGTCAAGATTTGAGAAATTTTAAATGAACCTGATATAGACTCGGAAGCC 1459
      |||||
Db 435 TTTAGTCAATTTGTTTGGATTTGAGAAATCCAAATTTATGTTTAAATAAAATTAATGGA 376
      |||||
QY 1460 ATATACGATAACAAACGACGTAAGGTGGACTGAGGAGACATAATAGATTCA 1515
      |||||
Db 375 TTTGAAAGAGAAATAGAGGATTCAAATCCATGGGATAAACACATATTATTATTA 320
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## RESULT 10

US-08-623-906A-18/c

; Sequence 18, Application US/08623906A

; Patent No. 5874217

; GENERAL INFORMATION:

; APPLICANT: Stevenson, Tamara

; APPLICANT: Dvorak, Jan

; APPLICANT: Halverson, Joy

; TITLE OF INVENTION: Microsatellite Sequences for Canine

; TITLE OF INVENTION: Genotyping

; NUMBER OF SEQUENCES: 60

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON &amp; HERBERT

; STREET: 4 Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: CA

; COUNTRY: US

; ZIP: 94111-4187

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/623,906A

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Sherwood, Pamela J.

; REGISTRATION NUMBER: 36,677

; REFERENCE/DOCKET NUMBER: A-62282/BIR

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-781-1989

; TELEFAX: 415-398-3249

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 376 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: 1..79

; OTHER INFORMATION: /note= "Nucleotides 1-79 are unique

; OTHER INFORMATION: flanking sequence"

; FEATURE:

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; NAME/KEY: misc feature
; LOCATION: 80..229
; OTHER INFORMATION: /note= "Nucleotides 80-229 are
; OTHER INFORMATION: repeat sequence"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 230..376
; OTHER INFORMATION: /note= "Nucleotides 230-376 are
; OTHER INFORMATION: unique flanking sequence"
; US-08-623-906A-18
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Query Match 1.0%; Score 45.4; DB 2; Length 376;

Best Local Similarity 47.7%; Pred. No. 0.06;

Matches 133; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

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QY 1013 AGATTTCTCAATTCGCTAGCTTCTGGTCTCTTTTCTTTTCATTCATGATCAAAAGCAA 1072
      |||||
Db 292 AGAAGCTCCAGATTTATTTATTTCTGTTCTTAAGTCATTAATCTCTCTCGA 233
      |||||
QY 1073 TCATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1132
      |||||
Db 232 ATCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 173
      |||||
QY 1133 ATTAATAATGGAATCTTTATCGAATCCAGCTCAATTTTGTTCCTTCTTCTTCTTCTTCT 1192
      |||||
Db 172 TTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 113
      |||||
QY 1193 TCTAAAGGTACTTAAGATGATTTATTCATGTCATGGTCTTCTTCTTCTTCTTCTTCTT 1252
      |||||
Db 112 TCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 113
      |||||
QY 1253 TGACTTGTATTTTGTTCGTTGATTTAGTGAATTT 1291
      |||||
Db 52 TATCCAAATTAATCCAAATTTTGAGAAATTCGTTATCTT 14
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## RESULT 11

US-07-867-106-2

; Sequence 2, Application US/07867106

; Patent No. 5389526

; GENERAL INFORMATION:

; APPLICANT: Slade, Martin B

; APPLICANT: Chang, Andy C M

; APPLICANT: Williams, Keith L

; TITLE OF INVENTION: Improved Plasmid Vectors for Cellular

; TITLE OF INVENTION: Slime Moulds of the Genus Dictyostellium

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &amp; No. 5389526ris

; STREET: One Liberty Place 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/867,106

; FILING DATE: 19920625

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: AU PJ 7187

; APPLICATION NUMBER: PCT/AU90/00530

; FILING DATE: 02-NOV-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: Feeney, Joanne Longo

; REGISTRATION NUMBER: 35,134

; REFERENCE/DOCKET NUMBER: RICE-0002

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-568-3100

; TELEFAX: 215-568-3439

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RESULT 12
US-09-395-604A-20/c
; Sequence 20. Application US/09395604A
; Patent No. 6458537
; GENERAL INFORMATION:
; APPLICANT: Staub, Rick W.
; APPLICANT: Carrico, Michael M.
; TITLE OF INVENTION: METHODS OF DNA TYPING WITH TANDEM
; TITLE OF INVENTION: REPEATS
; FILE REFERENCE: 062481.0107
; CURRENT APPLICATION NUMBER: US/09/395,604A
; CURRENT FILING DATE: 1999-09-14
; PRIOR APPLICATION NUMBER: 08/637,115
; PRIOR FILING DATE: 1996-04-24
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0

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RESULT 13  
5273901-6/c  
; Patent No. 5273901  
; APPLICANT: JACOBSON, JAMES W.; STRAUSBERG, ROBERT L.; WILSON,  
; SUSAN D.; POPE, SHARON H.; STRAUSBERG, SUSAN L.; RUFF, MICHAEL D.;  
; AUGUSTINE, PATRICIA C.; DANFORTH, HARRY D.  
; TITLE OF INVENTION: GENETICALLY ENGINEERED COCCIDIOSIS  
; SPOOROZITE 21.5 KB ANTIGEN, AC-6B  
; NUMBER OF SEQUENCES: 11  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/581,693  
; FILING DATE: 12-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 215,162  
; FILING DATE: 05-JUL-1988  
; APPLICATION NUMBER: 746,520  
; FILING DATE: 19-JUN-1985  
; APPLICATION NUMBER: 627,811  
; FILING DATE: 05-JUL-1984  
; SEQ ID NO: 6:  
; LENGTH: 543  
5273901-6

Query Match	1.0%	Score	44.4	DB	6	Length	543
Best Local Similarity	49.6%	Pred.	No.	0.12			
Matches	114	Conservative	0	Mismatches	116	Indels	0
Gaps	0						
QY	2975	GCTCTTTATAC	TGCGGCAACT	TTTGGCTCAT	CAATTTGGCTCCCGAT	TCTAGTGGTGC	3034
Db	242	GCTGCTGCTG	CTGCAGCTG	TGCTGTCAG	TGTGCTGCAGCTG	CGCTGGTGT	183
QY	3035	TCACCTGTTCC	AGGGAAC	TCACTCCGAA	TCTGGCTGCCAT	TGGCCGAGCCACT	3094
Db	182	GCTGTAGTCT	GCTGTTGCAG	CTGCTGTTGCT	GCTGCTGCTG	CTGCAGGTGCT	123
QY	3095	GCTGCTAGTCT	TGGTGGCTGC	CAATGGA	TATACCTTTAT	TGTGCTCCTC	3154
Db	122	GCTGTGCTG	CTGCAGT	GCTGCGCTCT	CTCTCTTTCTTT	CTCTCTCTCT	63
QY	3155	GGTGGTTTCA	CTAGTCA	TCTCCAT	CTACTTTTGG	ACCATCATGT	3204
Db	62	TCCTCTCTT	CTCTCTCT	CTCTCTCT	CTCTCTCTCT	CTCTCTCTCT	13

RESULT 14  
US-08-998-416-595

; Sequence 595, Application US/08998416  
; Patent No. 6239264  
; GENERAL INFORMATION:  
; APPLICANT: Philippsen, Peter  
; APPLICANT: Pohlmann, Rainer  
; APPLICANT: Steiner, Sabine  
; APPLICANT: Mohr, Christine  
; APPLICANT: Wendland, Jurgen  
; APPLICANT: Knechtle, Philipp  
; APPLICANT: Rebeschung, Corinne  
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPHII  
; TITLE OF INVENTION: AND USES THEREOF  
; NUMBER OF SEQUENCES: 1152  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6239264artis Corporation  
; STREET: 3054 Cornwalis Road  
; CITY: Research Triangle Park  
; STATE: No. 6239264ch Carolina  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/998,416  
; FILING DATE: 24-DEC-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: CH 0016/97  
; FILING DATE: 31-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8587  
; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 595:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 658 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORIGINAL SOURCE: PAG1408RP  
; ORGANISM: PAG1408RP  
; US-08-998-416-595

Query Match 1.0%; Score 43.2; DB 3; Length 658;  
Best Local Similarity 49.1%; Pred. No. 0.27;  
Matches 114; Conservative 0; Mismatches 118; Indels 0; Gaps 0;  
QY 1045 TTCTTTGTTTCAATCATCAAGCAAAATCTGGAATTAATAATGGAATCTTTATCGAATCCAAAGCT 1164  
Db 355 TTTATTTGTTGTTGTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 414  
QY 1105 ACTGTTTCTTATCCCAAGAAATCTGGAATTAATAATGGAATCTTTATCGAATCCAAAGCT 1164  
Db 415 ATTTATTTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 474  
QY 1165 GATTTGTTTCTTCAATGAAATCATCTCTAAAGGTACTTAAGATTTGATTTATTTATTTATTTATTT 1224  
Db 475 TGGTGACTTTATTTCAATATATATAGATTGATTTTGTGAACATAATATATATATGCTATTTCATA 534  
QY 1225 GGTCTTTCTTATTTGATGAATAAATGACTTGAATGATTTGTTTCTTTTCTTTTCTTTTCTTTTCT 1276  
Db 535 TTCTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 586

RESULT 15  
US-07-582-945-1/c

; Sequence 1, Application US/07582945  
; Patent No. 5369019  
; GENERAL INFORMATION:  
; APPLICANT: TAKER FOGED, Niels  
; APPLICANT: PETERSON, Svend  
; TITLE OF INVENTION: A PASTURELLA VACCINE  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/582,945  
; FILING DATE: 19901012  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 30307/112 PLVI  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4380 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORIGINAL SOURCE: Pasteurella multocida  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 219..4073  
; US-07-582-945-1

Query Match 1.0%; Score 42.2; DB 1; Length 4380;  
Best Local Similarity 50.2%; Pred. No. 1.1;  
Matches 130; Conservative 0; Mismatches 128; Indels 1; Gaps 1;  
QY 1031 AGCTTCTGCTCTCTTTCTTTCTTTGTTTCATTGATCAAAAGCA-AATCACTTCTTCTTCTTCT 1089  
Db 344 AACTCTTTCCATTTTTACATTTGTTTAATGCTTGTCTGAGATGATCAGTACACATCTTCT 285  
QY 1090 TCTTCTCGATTTCTTACTGTTTCTTTATCCACGAAATCTGGAATTAATAATGGAATCTTT 1149  
Db 284 AAAAAATTTTCATCGGCACTTTTCTCTTTTACAGTAAATCTGAGTTAAAAAATGTTTTGT 225  
QY 1150 TATCGAATCAAGCTGATTTTGTCTTTCTTTCATTGAATCATCTCTCTAAAGGTACTTAAGA 1209  
Db 224 TTTTCATATCAATCAACCTCTATGTTAGTTTATTTCTTAAAGTAAGATAATGCTTACTTAATA 165  
QY 1210 TTGATTTATTTGTCATGGTCTTTCTTTATTTGTTTGTGATGAATAAATGACTTCTGATTTGTTT 1269  
Db 164 AACATATTAATGATTTTGTGTTTATTAATAAACCACCAACATTCGAGTGTGGGTTTA 105  
QY 1270 GTTTTGTGATTAAGTGAAG 1288  
Db 104 TTTTGTGATTAATAA 86

Search completed: November 24, 2003, 13:07:50  
Job time : 239.433 secs



GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: November 23, 2003, 18:53:22 ; Search time 8051.27 Seconds  
 (without alignments)  
 11452.890 Million cell updates/sec

Title: US-10-084-553-3

Perfect score: 2254

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Scoring table: IDENTITY\_NUC

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

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3	1827	81.1	1827	6	AX506805	AX506805 Sequence
4	1805	80.1	2684	8	AY050961	AY050961 Arabidops
5	1612	71.5	1612	8	BT001096	BT001096 Arabidops
6	1612	71.5	1612	8	BT001105	BT001105 Arabidops
7	1527.6	67.8	4344	6	BD107660	BD107660 Phytochro
8	1527.6	67.8	5242	6	ATU79156	UT79156 Arabidopsis
9	1526.6	67.7	68415	8	AC005310	AC005310 Arabidops
10	223.4	9.9	318	8	AY166504	AY166504 Brassica
11	217.2	9.6	2526	6	A68428	A68428 Sequence 1
12	217.2	9.6	2526	8	ATAJ6404	AJ006404 Arabidops
13	213	9.4	1938	6	AX506421	AX506421 Sequence
14	202.2	9.0	2172	8	PVU420902	AJ420902 Phaseolus
15	189	8.4	1134	6	AX509497	AX509497 Sequence
16	137.6	6.1	1072	8	AY114070	AY114070 Arabidops
17	137.6	6.1	1429	8	AY063952	AY063952 Arabidops
18	117.6	5.2	2160	6	AX660076	AX660076 Sequence
19	112	5.0	451	6	AX660581	AX660581 Sequence
20	109.8	4.9	1317	6	AX658868	AX658868 Sequence
21	105.4	4.7	1638	6	AX658770	AX658770 Sequence
22	104.2	4.6	1332	8	AY087690	AY087690 Arabidops
23	104.2	4.6	1467	8	BT002002	BT002002 Arabidops
24	97.8	4.3	928	8	AY122969	AY122969 Arabidops
25	97.8	4.3	1427	8	AY091106	AY091106 Arabidops
26	94.8	4.2	2196	6	AX658772	AX658772 Sequence
27	90.4	4.0	999	6	AX658842	AX658842 Sequence
28	90	4.0	510	6	AX658822	AX658822 Sequence
29	81.6	3.6	86436	8	AC007323	AC007323 Genomic s
30	81.4	3.6	1051	8	AY081522	AY081522 Arabidops
31	81.4	3.6	1335	8	AY042894	AY042894 Arabidops
32	79.4	3.5	447	6	A68446	A68446 Sequence 19
33	75.4	3.3	666	6	A68433	A68433 Sequence 6
34	70	3.1	14826	8	AP004460	AP004460 Oryza sat
35	69	3.1	124212	8	AC126787	AC126787 Medicago
36	67.6	3.0	131006	2	AC137985	AC137985 Medicago
37	65.8	2.9	139490	8	AP003325	AP003325 Oryza sat
38	64.6	2.9	95327	8	AC013354	AC013354 Genomic s
39	64.6	2.9	96232	8	ATAC010927	AC010927 Arabidops
40	63	2.8	186315	8	OSJN00188	AL662987 Oryza sat
41	63	2.8	229796	2	AC137597	AC137597 Oryza sat
42	62.8	2.8	151517	2	AP005750	AP005750 Oryza sat
43	62.8	2.8	167114	2	AP004685	AP004685 Oryza sat
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## ALIGNMENTS

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 LOCUS  
 DEFINITION  
 Phytochrome regulated transcription factor for control of higher plant development.  
 ACCESSION  
 BD107661  
 VERSION  
 BD107661.1 GI:23202479  
 KEYWORDS  
 JP 2002501381-A/2.  
 SOURCE  
 unidentified  
 ORGANISM  
 unclassified  
 REFERENCE  
 1 (bases 1 to 2254)  
 Tobin, R., Sun, L. and Wang, Z.Y.  
 Phytochrome regulated transcription factor for control of higher plant development

BD107661 2254 bp DNA linear PAT 18-SEP-2002  
 Phytochrome regulated transcription factor for control of higher plant development.



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DEFINITION Arabidopsis thaliana DNA-binding protein CCA1 (CCA1) mRNA, complete cds.
ACCESSION U28422
VERSION U28422.1 GI:1777442
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
REFERENCE 1 Wang,Z.Y., Kenigsbuch,D., Sun,L., Harel,E., Ong,M.S. and Tobin,E.M.
AUTHORS A Myb-related transcription factor is involved in the phytochrome
TITLE regulation of an Arabidopsis lhcb gene
JOURNAL Plant Cell 9 (4), 491-507 (1997)
MEDLINE 97290202
PUBMED 914958
REFERENCE 2 Wang,Z.
AUTHORS Direct Submission
TITLE Submitted (06-JUN-1995) Zhiyong Wang, Dept. of Biology, University
JOURNAL of California at Los Angeles, 405 Hilgard Ave., Los Angeles, CA
90095, USA
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Db	2221	GTTTAAATCTTTTTTTTCCCA	2240
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LOCUS	AX506805	Sequence 1500 from Patent WO0216655.	
DEFINITION	AX506805		
ACCESSION	AX506805		
VERSION	AX506805.1	GI:23388042	
KEYWORDS			
SOURCE			
ORGANISM			
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		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	
REFERENCE			
AUTHORS		Harper, J.F., Kreps, J.J., Wang, X. and Zhu, T.	
TITLE		Stress-regulated genes of plants, transgenic plants containing same, and methods of use	
JOURNAL		Patent: WO 0216655-A 1500 28-FEB-2002;	
		The Scripps Research Institute (US) ; Syngenta Participations AG (CH)	
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## RESULT 4

AY050961

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

AY050961 2684 bp mRNA linear PLN 23-SEP-2002  
Arabidopsis thaliana At2g46830 mRNA sequence.  
AY050961.1 GI:15293054  
FLI CDNA.  
Arabidopsis thaliana (thale cress)  
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 2684)  
Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M.,  
Quach, H.L., Tang, C., Toriumi, M., Wallender, E.K., Wong, C., Wu, H.C.,  
Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y.,  
Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Natusaka, M.,  
Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P.,  
Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W.,  
Ecker, J.R. and Theologis, A.  
Arabidopsis Full Length cDNA Clones  
Unpublished  
2 (bases 1 to 2684)  
Yamada, K., Liu, S.X., Pham, P.K., Banh, J., Banno, F., Dale, J.M.,  
Goldsmith, A.D., Jiang, P.X., Lee, J.M., Onodera, C.S., Quach, H.L.,  
Tang, C.C., Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L.,  
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BT001105 1612 bp mRNA linear PLN 07-NOV-2002  
LOCUS Arabidopsis thaliana clone C105127 (D) putative MYB-related  
DEFINITION transcription factor CCAL1 (At2g46830) mRNA, complete cds.  
ACCESSION BT001105  
VERSION BT001105.1 GI:24762204  
KEYWORDS FLI CDNA  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
REFERENCE 1 (bases 1 to 1612)  
AUTHORS Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Chen,H., Cheuk,R., Jones,T., Kim,C.J., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Davis,R.W., Ecker,J.R. and Theologis,A.  
TITLE Arabidopsis Open Reading Frame (ORF) Clones  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1612)  
AUTHORS Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Chen,H., Cheuk,R., Jones,T., Kim,C.J., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Davis,R.W., Ecker,J.R. and Theologis,A.  
TITLE Direct Submission  
JOURNAL Submitted (07-NOV-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA  
COMMENT Annotation based on July 2002 version of the Arabidopsis genome submitted to Genbank.

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DEFINITION			
Phytochrome regulated transcription factor for control of higher			
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ACCESSION			
BD107660			
VERSION			
BD107660.1 GI:23202478			
KEYWORDS			
JP 2002501381-A/1.			
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REFERENCE			
1 (bases 1 to 4344)			
Tobin,R., Sun,L. and Wang,Z.Y.			
Phytochrome regulated transcription factor for control of higher			
plant development			
JOURNAL			
Patent: JP 2002501381-A 1 15-JAN-2002;			
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA			
COMMENT			
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PR 18-APR-1997 US 08/843572			
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PC C12N15/00, C12N15/09, C12N15/29, C12N15/82, A01H1/00, A01H3/00, PC			
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FT source			
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Location/Qualifiers			



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LOCUS      Arabidopsis thaliana Myb-related transcription factor CCA1 gene,
DEFINITION complete cds.
ACCESSION U79156
VERSION   U79156.1 GI:4090568
KEYWORDS
SOURCE    Arabidopsis thaliana (thale cress)
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           1 (bases 1 to 5242)
REFERENCE Wang,Z.Y., Kenigsbuch,D., Sun,L., Harel,E., Ong,M.S. and Tobin,E.M.
AUTHORS   A Myb-related transcription factor is involved in the phytochrome
TITLE     regulation of an Arabidopsis lhcb gene
JOURNAL   Plant Cell 9 (4), 491-507 (1997)
MEDLINE   97290202
PUBMED    9144958
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AUTHORS   2 (bases 1 to 5242)
TITLE     Direct Submission
JOURNAL   Submitted (21-NOV-1996) MCD Biology, University of California at
          Los Angeles, 405 Hilgard, Los Angeles, CA 90095, USA
          Location/Qualifiers
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RESULT 10
AY166504
LOCUS
DEFINITION
Brassica rapa subsp. pekinensis Myb-related transcription factor
CCAL mRNA, partial cds.
ACCESSION
AY166504
VERSION
AY166504.1 GI:27357049
SOURCE
Brassica rapa subsp. pekinensis
ORGANISM
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
FEATURES
1. (bases 1 to 318)
REFERENCE
Jang,H. and Hur,Y.
AUTHORS
Study on the expression pattern of genes associated with flowering
TITLE
in chinese cabbage plants
JOURNAL
Unpublished
REFERENCE
2. (bases 1 to 318)
AUTHORS
Jang,H. and Hur,Y.
TITLE
Direct Submission
JOURNAL
Submitted (16-OCT-2002) Biology, Chungnam National University,
Kungdong, Yuseong-ku, Deajeon 305-764, Korea
LOCATION/Qualifiers
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KEYWORDS
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1. (bases 1 to 2526)
REFERENCE
Coupland,G.M. and Schaffer,R.J.
AUTHORS
GENETIC CONTROL OF FLOWERING
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Patent: WO 9749811-A 1 31-DEC-1997;
JOURNAL
INNES JOHN CENTRE INNOV LTD (GB)
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
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#### SUMMARIES

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#### ALIGNMENTS

#### RESULT 1

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; Publication No. US20030056247A1  
; GENERAL INFORMATION:  
; APPLICANT: Tobin, Elaine  
; APPLICANT: Wang, Zhi-Yong  
; APPLICANT: Sun, Lin  
; TITLE OF INVENTION: The Regents of the University of California  
; TITLE OF INVENTION: Phytochrome Regulated Transcription Factor for Control  
; FILE REFERENCE: 023070-124200US  
; CURRENT APPLICATION NUMBER: US/10/084,553  
; CURRENT FILING DATE: 2002-07-09  
; PRIOR APPLICATION NUMBER: US 08/843,572  
; PRIOR FILING DATE: 1997-04-18  
; NUMBER OF SEQ ID NOS: 27  
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3661 ATATAAATATGTFACATTTCGGGTGCAATGCTTCCAGCTCTCTTCTCCAGAGAGGTAT 3720  
3661 ATATAAATATGTFACATTTCGGGTGCAATGCTTCCAGCTCTCTTCTCCAGAGAGGTAT 3720  
3721 TGCCCAAGATTTTACATATCGAGAGAAACACAGAGAGAGAAACAAACAAACAAAGAAC 3780  
3721 TGCCCAAGATTTTACATATCGAGAGAAACACAGAGAGAGAAACAAACAAACAAAGAAC 3780  
3781 AAAGATATCCAAATGGCACTTGAATCTTAACTTCAAGCTCAGTTTAAACACAGCTTGAATC 3840  
3781 AAAGATATCCAAATGGCACTTGAATCTTAACTTCAAGCTCAGTTTAAACACAGCTTGAATC 3840  
3841 AAGAGGAGAGAGAAACACAGAGTTTCTTGGAAATCGGATTAAGTTCCTTCAAGAGCTTAAGA 3900  
3841 AAGAGGAGAGAGAAACACAGAGTTTCTTGGAAATCGGATTAAGTTCCTTCAAGAGCTTAAGA 3900  
3901 GTAGGAGAGAGAACAGGTTTAAACCAATACAAAAGATGTTTCCATGGAAGCCAAAGAAAGTA 3960

Db 3901 GTAGAGGAACACAGGTTTTTAAACCACATACAAAGATGTTCCATGGAAGCCAAAGAGTA 3960  
Qy 3961 GAATCTCAACAAATCCTTATCATTCATGTGGAACAGAAAGATCCCAACGGATGCGGT 4020  
Db 3961 GAATCTCTCAACAAATCCTTATCATTCATGTGGAACAGAAAGATCCCAACGGATGCGGT 4020  
Qy 4021 TGGAAACTCAAGCTTCCACATGAGACTCTATTTTCATCTGATCTGTTGTTGTACTCTGT 4080  
Db 4021 TGGAAACTCAAGCTTCCACATGAGACTCTATTTTCATCTGATCTGTTGTTGTACTCTGT 4080  
Qy 4081 TTTTAAGTTTTCAGACCACTGTCTACATTTCTTTCTTTCTTTGAGGCCCTTTGTTATTTGTT 4140  
Db 4081 TTTTAAGTTTTCAGACCACTGTCTACATTTCTTTCTTTCTTTGAGGCCCTTTGTTATTTGTT 4140  
Qy 4141 TCCTTGTCATAGCTTCTCTGTACATTTTCAGCTCTGATTTATTTATTCACAAATCATAACTG 4200  
Db 4141 TCCTTGTCATAGCTTCTCTGTACATTTTCAGCTCTGATTTATTTATTCACAAATCATAACTG 4200  
Qy 4201 TTTTAATCTTTTTCACCTCGGAAGAACTTCACTCAAGGGGCTCTTTGTTCTTGATA 4260  
Db 4201 TTTTAATCTTTTTCACCTCGGAAGAACTTCACTCAAGGGGCTCTTTGTTCTTGATA 4260  
Qy 4261 TATGCAAAACAGAGAGTTCCAAACGTAATCTTTAGCCCATCCATCAACCTTAAAGTTGCT 4320  
Db 4261 TATGCAAAACAGAGAGTTCCAAACGTAATCTTTAGCCCATCCATCAACCTTAAAGTTGCT 4320  
Qy 4321 CATAACTCATAAGTAAGCACAAA 4344  
Db 4321 CATAACTCATAAGTAAGCACAAA 4344

## RESULT 2

US-10-084-553-3  
; Sequence 3, Application US/10084553  
; Publication No. US20030056247A1  
; GENERAL INFORMATION:  
; APPLICANT: Tobin, Elaine  
; APPLICANT: Wang, Zhi-Yong  
; APPLICANT: Sun, Lin  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Phytochrome Regulated Transcription Factor for Control  
; FILE REFERENCE: 023070-124200US  
; CURRENT APPLICATION NUMBER: US/10/084,553  
; CURRENT FILING DATE: 2002-07-09  
; PRIOR APPLICATION NUMBER: US 08/843,572  
; PRIOR FILING DATE: 1997-04-18  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 2254  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:full-length  
; OTHER INFORMATION: CCA1 cDNA clone 25 constructed joining 5' and 3'  
; OTHER INFORMATION: fragments of clones 21 and 24  
US-10-084-553-3

Query Match 35.2%; Score 1527.6; DB 14; Length 2254;  
Best Local Similarity 87.9%; Pred. No. 0;  
Matches 1803; Conservative 0; Mismatches 9; Indels 240; Gaps 3;  
Qy 2180 TCTCTCTCAGTAGAGAAAGAGCTGAAGCTAAAGGTAGTACTATGGGTCAAGCGGTAGA 2239  
Db 441 TTTTCCAGGTAGAGAAAGAGCTGAAGCTAAAGGTAGTACTATGGGTCAAGCGGTAGA 500  
Qy 2240 CATAGCTATTCTCTCCACGGCTTAAGCGTAAACCAAACTTATCTCTCGAAAGAC 2299  
Db 501 CATAGCTATTCTCTCCACGGCTTAAGCGTAAACCAAACTTATCTCTCGAAAGAC 560  
Qy 2300 GGAAGTGGAACGATCTTATGTCAAAAACGGGTGTGAATGATGGAAGAGTCCCTTGG 2359

Db 561 GGAAGTGGAACGATCTTATGTCAAAAACGGGTGTGAATGATGGAAGAGTCCCTTGG 620  
Qy 2360 ATCAGAAAAAGTGTGCGATCTCTGAGGTGATTTTCAATGGTCATATGGCATCTTTTTTGCAGT 2419  
Db 621 ATCAGAAAAAGTGTGCGATCTCTG----- 643  
Qy 2420 GTGTCACATGCTCTCTCATGTTATTATAACAGATTGTGCTGCTTTATAGATGGCCAA 2479  
Db 644 -----AGATGGCCAA 653  
Qy 2480 TGAAGATCGACAACAATCAAAAGCTGAAGAGAAAACTCTCGAGGAAGACAACCTGTTGAGA 2539  
Db 654 TGAAGATCGACAACAATCAAAAGCTGAAGAGAAAACTCTCGAGGAAGACAACCTGTTGAGA 713  
Qy 2540 TTGTTTCACTCATCATGATATCTCTGCTGATCTCTCATGATTAATAAGTTGTATAGAGAC 2599  
Db 714 TTGTTTCACTCATCATGATATCTCTGCTGATCTCTCATGATTAATAAGTTGTATAGAGAC 773  
Qy 2600 ATCAAAACGCAAGCACCTTCCGCGAGTTCTTGGCCCTTACGGGAAG----- 2659  
Db 774 ATCAAAACGCAAGCACCTTCCGCGAGTTCTTGGCCCTTACGGGAAG----- 817  
Qy 2660 TTCAATTGCTATTTCAGGTTTTTAAGACGATTAGTACTTTTCATGAAACTAAAAACCGTGGG 2719  
Db 818 ----- 817  
Qy 2720 GAATAACAGGAAGTCAAGATAACAGGGTAAGAAAGAGTCAAACTCAGATTTCGAATGCA 2779  
Db 818 -----AGGGAAGTCAGAAATAACAGGGTAAGAAAGAGTCAAACTCAGATTTCGAATGCA 870  
Qy 2780 AAATCTCTGCAAAACGTTATGACGAGGACCTCAGACTTATCCGATGCATATCCCTGTG 2839  
Db 871 AAATCTCTGCAAAACGTTATGACGAGGACCTCAGACTTATCCGATGCATATCCCTGTG 930  
Qy 2840 CTAGTGCCATTGGGGAGCTCAATAACAAAGTTCTCTATCAGATCTCTCTCAGAGCCAGAT 2899  
Db 931 CTAGTGCCATTGGGGAGCTCAATAACAAAGTTCTCTATCAGATCTCTCTCAGAGCCAGAT 990  
Qy 2900 AGTCATCCCCACACAGTTGCGAGGATATCAGTCTGTTTCTTAATATATATATGTCACCC 2959  
Db 991 AGTCATCCCCACACAGTTGCGAGGATATCAGTCTGTTTCTTAATATATATGTCACCC 1050  
Qy 2960 CTTTTCAACACACCGGCTCTTTTACTGCGCAACTTTTCGCTCATCATTTTGGCGCTCCC 3019  
Db 1051 CTTTTCACAAACACCGGCTCTTTTACTGCGCAACTTTTCGCTCATCATTTTGGCGCTCCC 1110  
Qy 3020 GATTCTAGTGTGGCTCACCTGTTCCAGGGAACCTCACCTCCGAATCTGGGTGCCATGGCC 3079  
Db 1111 GATTCTAGTGTGGCTCACCTGTTCCAGGGAACCTCACCTCCGAATCTGGGTGCCATGGCC 1170  
Qy 3080 GCAGCCACTGTTGCGAGCTGCTAGTGTGTTGGGCTGCCAATGGATTATTACCTTTATGT 3139  
Db 1171 GCAGCCACTGTTGCGAGCTGCTAGTGTGTTGGGCTGCCAATGGATTATTACCTTTATGT 1230  
Qy 3140 GCTCTCTTATAGTTTCAAGTGTGTTTCACTAGTCATCTCTCATCTCTTTTGGACCATCATGT 3199  
Db 1231 GCTCTCTTATAGTTTCAAGTGTGTTTCACTAGTCATCTCTCATCTCTTTTGGACCATCATGT 1290  
Qy 3200 GATTGTAGGTACAAAAAGCAAGCACCTTTACAAACATGGTTCTGTGAGAGCCGAGAGCAA 3259  
Db 1291 GATTGTAGGTACAAAAAGCAAGCACCTTTACAAACATGGTTCTGTGAGAGCCGAGAGCAA 1350  
Qy 3260 GAACACTCCGAGGCATCAAGGCTCGATCTTCACTGGACTCAGAGGATGTTGAAAAAAG 3319  
Db 1351 GAACACTCCGAGGCATCAAGGCTCGATCTTCACTGGACTCAGAGGATGTTGAAAAAAG 1410  
Qy 3320 AGTAAACCAAGTTTGTATGAGAGCCCTTCTGCAACACCTCAGAGTGTGCAAGGGTTCA 3379  
Db 1411 AGTAAACCAAGTTTGTATGAGAGCCCTTCTGCAACACCTCAGAGTGTGCAAGGGTTCA 1470  
Qy 3380 GATGGAGCAGGAGACAGAAAAAAGTTGACCGGTCTCTGTTGGCTCAAAACACTCCGTGCG 3439





Db 1051 CTTTAAACAACCGGCTCTTTATCTGCGCAACTTTGCGCTCATCAITTTTGGCCTCCC 1110  
Qy 3020 GATTCTAGTGGGCTCACTGTTCCAGGAACCTCACTCCGAATCTGGCTGCCATGGCC 3079  
Db 1111 GATTCTAGTGGGCTCACTGTTCCAGGAACCTCACTCCGAATCTGGCTGCCATGGCC 1170  
Qy 3080 GCAGCCACTGTTCCAGCTGCTAGTGTGTTGGTGGCTGCCAATGGATTATTACCTTTATGT 3139  
Db 1171 GCAGCCACTGTTCCAGCTGCTAGTGTGTTGGTGGCTGCCAATGGATTATTACCTTTATGT 1230  
Qy 3140 GCTCCTCTTAGTTCAAGTGGTTTCACTAGTCAATCTCTCACTCTCTCTTTTGGACCATCATGT 3199  
Db 1231 GCTCCTCTTAGTTCAAGTGGTTTCACTAGTCAATCTCTCTCTCTCTTTTGGACCATCATGT 1290  
Qy 3200 GATGTAGTACACAAAAGCAAGCACTTTACACATGTTCTGTGAGAGCCGAGAGCAA 3259  
Db 1291 GATGTAGTACACAAAAGCAAGCACTTTACACATGTTCTGTGAGAGCCGAGAGCAA 1350  
Qy 3260 GAACACTCCGAGGCATCAAAAGGCTCGATCTTCACTGGACTCAGAGGATGTTGAAAATAAG 3319  
Db 1351 GAACACTCCGAGGCATCAAAAGGCTCGATCTTCACTGGACTCAGAGGATGTTGAAAATAAG 1410  
Qy 3320 AGTAAACCAAGTTTGTATGAGAGCCTTCTGCAACACCTGAGAGTGATGCAAAAGGTTCA 3379  
Db 1411 AGTAAACCAAGTTTGTATGAGAGCCTTCTGCAACACCTGAGAGTGATGCAAAAGGTTCA 1470  
Qy 3380 GATGGAGCAGGACAGAAAAGTGTGACCGTCTCTGTGGCTCAACACCTCGTGG 3439  
Db 1471 GATGGAGCAGGACAGAAAAGTGTGACCGTCTCTGTGGCTCAACACCTCGTGG 1530  
Qy 3440 AGTAGTGATGATGTTGAGCGGATGTCATCAGAAAGGCAAGAGATGGCACCAATGTTGAG 3499  
Db 1531 AGTAGTGATGATGTTGAGCGGATGTCATCAGAAAGGCAAGAGATGGCACCAATGTTGAG 1590  
Qy 3500 GTGAAAGAAACGAATGAAGACACTATAAACCCTCAAACTTCAGAGTCCAATGCACCCGC 3559  
Db 1591 GTGAAAGAAACGAATGAAGACACTATAAACCCTCAAACTTCAGAGTCCAATGCACCCGC 1650  
Qy 3560 AGTAGAATCAGCTCCCAATATAACCGATCCTAGTGAAGTCTGTGCTCAGAGGTACTTACT 3619  
Db 1651 AGTAGAATCAGCTCCCAATATAACCGATCCTAGTGAAGTCTGTGCTCAGCA----- 1700  
Qy 3620 TGGACTAAAGATCAACTTCTTTATTTCAAATCATTTTCTCATATAAATATTGTACATTC 3679  
Db 1701 ----- 1700  
Qy 3680 GGGTCGAATTGCTTCCAGCTCTCTTCTCCAGAGAGGTATTGCGCGAAAGTTTTACATA 3739  
Db 1701 GGGTCGAATTGCTTCCAGCTCTCTTCTCCAGAGAGGTATTGCGCGAAAGTTTTACATA 1760  
Qy 3740 TCGAAGAAACACAGAGAGGAAGAAACAAACAAACAAAGAGATATCCCAATGGCACT 3799  
Db 1761 TCGAAGAAACACAGAGAGGAAGAAACAAACAAAGAAAGATATCCCAATGGCACT 1820  
Qy 3800 TGATCTTAACTTCAAGCTCAGTTAAACACAGTTGATGATCAAGAGGAGAGAGAAACAC 3859  
Db 1821 TGATCTTAACTTCAAGCTCAGTTAAACACAGTTGATGATCAAGAGGAGAGAGAAACAC 1880  
Qy 3860 AGGATTTCTTGGNAATCGGATTAGATGCTTCAAGCTTAATGAGTAGAGGAAGAACAGTTT 3919  
Db 1881 AGGATTTCTTGGNAATCGGATTAGATGCTTCAAGCTTAATGAGTAGAGGAAGAACAGTTT 1940  
Qy 3920 TAAACCATACAAAGATGTTCCATGGAAGCCAAAGAAAGTAGAATCCTCAACAAACATCC 3979  
Db 1941 TAAACCATACAAAGATGTTCCATGGAAGCCAAAGAAAGTAGAATCCTCAACAAACATCC 2000  
Qy 3980 TATCATTTATGGAACAGAAAGATCCCAACCGATGCGGTTGGAACTCAAGCTTTCCAC 4039  
Db 2001 TATCATTTATGGAACAGAAAGATCCCAACCGATGCGGTTGGAACTCAAGCTTTCCAC 2060  
Qy 4040 ATGAGACTCTATTTTTCATCTGCTGTTGTTGCTTCTGTTTAAAGTTTTCAAGACCA 4099

Db 2061 ATGAGACTCTATTTTTCATCTGATCTGTTTGTACTCTGTTTAAAGTTTTCAAGACCA 2120  
Qy 4100 CTGCTACATTTCTTTTCTTTTGGAGCCCTTGTATTTGTTCTCTTGTGCATAGTCTTCC 4159  
Db 2121 CTGCTACATTTCTTTTCTTTTGGAGCCCTTGTATTTGTTCTCTTGTGCATAGTCTTCC 2180  
Qy 4160 TGTAAACATTTGACTCTGTATTTTCAACAAATCATAAACTGTTTAAATCTTTTTTTTCCA 4219  
Db 2181 TGTAAACATTTGACTCTGTATTTTCAACAAATCATAAACTGTTTAAATCTTTTTTTTCCA 2240

RESULT 4  
US-09-938-842A-1500  
; Sequence 1500, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; FILE REFERENCE: SAME, AND METHODS OF USE  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 1500  
; LENGTH: 1827  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-1500

Query Match 31.1%; Score 1349.2; DB 10; Length 1827;  
Best Local Similarity 87.0%; Pred. No. 0;  
Matches 1621; Conservative 0; Mismatches 3; Indels 240; Gaps 3;

Qy 2180 TCTCTCTCAGGTAGAGAAAGAGGCTGAAGCTAAAGGTGTAGCTATGGGTCAAGCGCTAGA 2239  
Db 204 TTTCTCAAGGTAGAGAAAGAGGCTGAAGCTAAAGGTGTAGCTATGGGTCAAGCGCTAGA 263  
Qy 2240 CATAGCTATTCTCTCTCCACGGCTTAAGCGTAAACCAACAATCCTTATCTCTCGAAAGAC 2299  
Db 264 CATAGCTATTCTCTCTCCACGGCTTAAGCGTAAACCAACAATCCTTATCTCTCGAAAGAC 323  
Qy 2300 GGGAGTGAACGATCCTTATGTCAAAAAGGGGTGAATGATGGAAGAGTCCCTTGG 2359  
Db 324 GGGAGTGAACGATCCTTATGTCAAAAAGGGGTGAATGATGGAAGAGTCCCTTGG 383  
Qy 2360 ATCAGAAAAGTGTCCGATCCTCGAGGTGATTTTCATGGTGCATATGTCATCTTTTTCAGT 2419  
Db 384 ATCAGAAAAGTGTCCGATCCTG----- 406  
Qy 2420 GTGTACATGTCTCTCATGTTATTAAATACAGATTGTGTCTTCGTTTATAGATGCCAA 2479  
Db 407 -----AGATGCCAA 416  
Qy 2480 TGAAGATCGACAAACATCAAGCCCTGAAGAGAAAACCTCTGCAGGAAGACAACTGTTTCA 2539  
Db 417 TGAAGATCGACAAACATCAAGCCCTGAAGAGAAAACCTCTGCAGGAAGACAACTGTTTCA 476  
Qy 2540 TTGTTTCACTCATCAGTATCTCTCTGCTCATCTCCATGAAATATAAGTTGTATAGAGAC 2599  
Db 477 TTGTTTCACTCATCAGTATCTCTCTGCTCATCTCCATGAAATATAAGTTGTATAGAGAC 536  
Qy 2600 ATCAAAACGCAAGCACTTTCCGCGAGTTTTCGCTTTCACGGGAAGAGGTAAAAAACAATCT 2659  
Db 537 ATCAAAACGCAAGCACTTTCCGCGAGTTTTCGCTTTCACGGGAAG----- 580

Qy	2660	TTCAATTGCTATTTCGAGGTTTTTAAGACGATTAGTAGTACTTTTCATGAAACTAAAAACGTCGGG	2719
Db	581	-----	580
Qy	2720	GAATAACAGGGAAGTTCAGAATAACAGGGTAAGAAAGGAGTCAAACTCAGATTTTGAATGCA	2779
Db	581	-----AGGGAAGTCAAGAATAACAGGGTAAGAAAGGAGTCAAACTCAGATTTGAATGCA	633
Qy	2780	AAATCTCTGGAAAAACGGTAATGACGACAGGACCTCAGACTTATCCGATGCAATATCCCTGTG	2839
Db	634	AAATCTCTGGAAAAACGGTAATGACGACAGGACCTCAGACTTATCCGATGCAATATCCCTGTG	693
Qy	2840	CTAGTGCCATTGGGAGCTCAATAACAAAGTTCTCTATCACATCCTCTCAGAGCCAGAT	2899
Db	694	CTAGTGCCATTGGGAGCTCAATAACAAAGTTCTCTATCACATCCTCTCAGAGCCAGAT	753
Qy	2900	AGTCATCCCCACACAGTTGCGAGGAGTATATCAGTCGTTTCTTAATCATATAATGTCAACC	2959
Db	754	AGTCATCCCCACACAGTTGCGAGGAGTATATCAGTCGTTTCTTAATCATATAATGTCAACC	813
Qy	2960	CTTTTACAACACACGGCTCTTTATCTATGCGCGAACTTTTGGCTCATCATTTTGGCCTCCC	3019
Db	814	CTTTTACAACACACGGCTCTTTATCTATGCGCGAACTTTTGGCTCATCATTTTGGCCTCCC	873
Qy	3020	GATTCTAGTGTGCTCACCTGTTTCCAGGGAACCTCACCTCGAATCTGGCTGCCATGGCC	3079
Db	874	GATTCTAGTGTGCTCACCTGTTTCCAGGGAACCTCACCTCGAATCTGGCTGCCATGGCC	933
Qy	3080	GCAGCCACTGTTGCGAGCTGTAGTGCTTGTGTGGCTGCCAATGGATTATTACCTTTATGT	3139
Db	934	GCAGCCACTGTTGCGAGCTGTAGTGCTTGTGTGGCTGCCAATGGATTATTACCTTTATGT	993
Qy	3140	GCTCCTCTTAGTTCAAGTGGTTTCACCTAGTCATCCTCCATCTACTTTTGGACCATCATGT	3199
Db	994	GCTCCTCTTAGTTCAAGTGGTTTCACCTAGTCATCCTCCATCTACTTTTGGACCATCATGT	1053
Qy	3200	GATGTAGAGTACAAAAAGCAAGCACTTTACAACATGTTCTGTGCAGAGCCGAGAGCAA	3259
Db	1054	GATGTAGAGTACAAAAAGCAAGCACTTTACAACATGTTCTGTGCAGAGCCGAGAGCAA	1113
Qy	3260	GAACACTCCGAGGCATCAAAAGGCTCGATCTTCACTGGACTCAGAGGATGTTGAAATTAAG	3319
Db	1114	GAACACTCCGAGGCATCAAAAGGCTCGATCTTCACTGGACTCAGAGGATGTTGAAATTAAG	1173
Qy	3320	AGTAAACAGTTTGTCTATGACGACCTTCTGCAACACCTCAGAGTGTGAAAGGGTTCA	3379
Db	1174	AGTAAACAGTTTGTCTATGACGACCTTCTGCAACACCTCAGAGTGTGAAAGGGTTCA	1233
Qy	3380	GATGGACGAGAGACAGAAAACAAGTTGACCGGTCCTCGTGTGGCTCAAAACCTCCGTCG	3439
Db	1234	GATGGACGAGAGACAGAAAACAAGTTGACCGGTCCTCGTGTGGCTCAAAACCTCCGTCG	1293
Qy	3440	AGTAGTGATGATGTTGAGGCGGATGCAATAGAAAGCAAGGATGGCAATGTTGAG	3499
Db	1294	AGTAGTGATGATGTTGAGGCGGATGCAATAGAAAGCAAGGATGGCAATGTTGAG	1353
Qy	3500	GTGAACAAACCAATGAAGACACTTAATAAACCTTCAAGTCCCAATGCAACGCCGC	3559
Db	1354	GTGAACAAACCAATGAAGACACTTAATAAACCTTCAAGTCCCAATGCAACGCCGC	1413
Qy	3560	AGTAGAATCAGCTCCCAATATAACCGATGCCATGGAAGTCTGTGTGACGAGGTACTTACT	3619
Db	1414	AGTAGAATCAGCTCCCAATATAACCGATGCCATGGAAGTCTGTGTGACGAGGTACTTACT	1463
Qy	3620	TGGACTAAAGATCAACTTCCTTTATTTTCAAATCAATTTTCTCATATAAATATTGTACATTC	3679
Db	1464	-----	1463
Qy	3680	GGGTCCGAATTGCCTTCCAGCTCTCTCTCCAGAGAGGTATTGCCGCAAGTTTTCATA	3739
Db	1464	GGGTCCGAATTGCCTTCCAGCTCTCTCTCCAGAGAGGTATTGCCGCAAGTTTTCATA	1523

## RESULT 5

US-09-887-576-702

: Sequence 702: Application IIS/09887576

: Patent No. US20020144047A1  
: Sequence 702, Application; PACIFIC NO. US2002014  
: GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: BUDWORTH, BROWN D

APPLICANT: BROWN, D  
APPLICANT: CHANG, H

APPLICANT: Chang, H

APPLICANT: Zhu, T.

APPLICANT: Han, B.  
APPLICANT: W...

APPLICANT: Wang, X.

APPLICANT: Cooper, Bret

; TITLE OF INVENTION: Promote

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; FILE REFERENCE: 1360.001US1

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; CURRENT APPLICATION NUMBER: US/0

; CURRENT FILING DATE: 2001-06-25

; PRIOR APPLICATION NUMBER: US

; PRIOR FILING DATE: 2000-06-23

; PRIOR APPLICATION NUMBER: US 60/214,087

; PRIOR FILING DATE: 2000-06-23

; PRIOR APPLICATION NUMBER: US

; PRIOR FILING DATE: 2000-1

; NUMBER OF SEQ ID NOS: 875

; SOFTWARE: Fast

; SEQ ID NO 702

; LENGTH: 1:

LENGTH: 1137  
TYPE: DNA

TYPE: DNA  
ORGANISM: Arabidopsis thaliana

	Query Match	26.2%	Score 1137;	DB 10;	Length 1137;
	Best Local Similarity	100.0%;	Pred. No. 3.6e-273;	Mismatches 0;	Gaps 0;
	Matches 1137;	Conservative 0;			
QY	198	ATCAAAAGGGAAGAAGAAGAAGCCCTTTTGGGCCATTTCATGAATTCGAATGAA	255		
Db	1	ATCAAAAGGGAAGAAGAAGAAGCCTTTTTGAGGCCATTTCATGAATTCGAATGAA	60		
QY	258	GGATATCAAAGAATCTAACACAAGGCCACGTCTTCCTCAATCTTTCCTCTTGTA	317		
Db	61	GGATATCAAAGAATCTAACACAAGGCCACGTCTTCCTCAATCTTTCCTCTTGTA	120		
QY	318	CTAATAATTTTCATCCTTTCTCTCTCTGTCTCTGGTCTTTTAGCTCAAAGTATCA	377		
Db	121	CTAATAATTTTCATCCTTTCTCTCTCTGTCTCTGGTCTTTTAGCTCAAAGTATCA	180		
QY	378	TCCATTATGTCAAAGTGTTGAAATTCCTCAAGACTATATGAGATGTTTGTGTTTCAT	437		

Db	181	TCCATTATATGTCAAAGTGTTGTTAAATTCCTCAAGACTATATATGAGATGTTTGTGTTTCAT	240
Qy	438	TTTCCAAATTTCAAACCTTTGFCGCCATTTAGTCTTCTACCCCTTCATCATGTTAGCTT	497
Db	241	TTTCCAAATTTCAAACCTTTGFCGCCATTTAGTCTTCTACCCCTTCATCATGTTAGCTT	300
Qy	498	AGCTTAATGCTGAACGTGTTGAATACGATATGGGCCCTTATGCTAAAGAAACAAACCTTA	557
Db	301	AGCTTAATGCTGAACGTGTTGAATACGATATGGGCCCTTATGCTAAAGAAACAAACCTTA	360
Qy	558	TGGGTCTAAAAAATAAAGCCCAATATAAAACTATGGCCCAATAAAGTTTAGTGCCATT	617
Db	361	TGGGTCTAAAAAATAAAGCCCAATATAAAACTATGGCCCAATAAAGTTTAGTGCCATT	420
Qy	618	GAGTGTGAGAAATAGCGCGTGTAGTGAAACGGACAGAAATGCGCGTTTCGATTTGGTGAA	677
Db	421	GAGTGTGAGAAATAGCGCGTGTAGTGAAACGGACAGAAATGCGCGTTTCGATTTGGTGAA	480
Qy	678	GTAGTGTCTAGATTTCCCGGGTCCACTGATGTTTCTAGTGTATCAGACACGTGTCGAA	737
Db	481	GTAGTGTCTAGATTTCCCGGGTCCACTGATGTTTCTAGTGTATCAGACACGTGTCGAA	540
Qy	738	ACTGTTGGAGAGATTAAAGATCTTTAAGTAGTCCCACTAGATCAAGATATTTATAACGAA	797
Db	541	ACTGTTGGAGAGATTAAAGATCTTTAAGTAGTCCCACTAGATCAAGATATTTATAACGAA	600
Qy	798	TTGACCTTTTTAAACCTTTTCAGTAGTCCCGAACTCGTGGCTTAGAATACAAAGAGGTT	857
Db	601	TTGACCTTTTTAAACCTTTTCAGTAGTCCCGAACTCGTGGCTTAGAATACAAAGAGGTT	660
Qy	858	GTGAACAAAGTTGATGTTTAAGATGGACAAGAAATGTAACCTTGAAACAAAAGCTCAATC	917
Db	661	GTGAACAAAGTTGATGTTTAAGATGGACAAGAAATGTAACCTTGAAACAAAAGCTCAATC	720
Qy	918	TTGAGCCACTAGTATGTTTGACATATGGCAGATTTCTTTTGTAGCCCTCGAAATAAATAAT	977
Db	721	TTGAGCCACTAGTATGTTTGACATATGGCAGATTTCTTTTGTAGCCCTCGAAATAAATAAT	780
Qy	978	AAAAAGTTTGAGGTTAAAGATAATATAGTGGCTGAGATTTCTCCATTTCCGTAGCTTCT	1037
Db	781	AAAAAGTTTGAGGTTAAAGATAATATAGTGGCTGAGATTTCTCCATTTCCGTAGCTTCT	840
Qy	1038	GGTCTCTTTCTTTGTTTCATGTACAAAGCAATCACCTTCTTCTTCTTCTTCTCTCG	1097
Db	841	GGTCTCTTTCTTTGTTTCATGTACAAAGCAATCACCTTCTTCTTCTTCTTCTCTCG	900
Qy	1098	ATTTCTTACTGTTTCTTTATCCAACGAAATCTGGAATTTAAAAATGGAATCTTTATCGAAT	1157
Db	901	ATTTCTTACTGTTTCTTTATCCAACGAAATCTGGAATTTAAAAATGGAATCTTTATCGAAT	960
Qy	1158	CCAAGCTGATTTTGTTCCTTTTCATGTAATCATCTCTCTAAAGGTACTTTAAGATTGATTA	1217
Db	961	CCAAGCTGATTTTGTTCCTTTTCATGTAATCATCTCTCTAAAGGTACTTTAAGATTGATTA	1020
Qy	1218	TTGTCAATGGTCTTCTTATTTGTTTGATGAATAAATCTGACTTGATTTGTTTTGTTTGTG	1277
Db	1021	TTGTCAATGGTCTTCTTATTTGTTTGATGAATAAATCTGACTTGATTTGTTTTGTTTGTG	1080
Qy	1278	GATTAGTGGAAATTTTGTAAAGAGAAGATCTGAAGTTGTGTAGAGAGCTTAGTGATG	1334
Db	1081	GATTAGTGGAAATTTTGTAAAGAGAAGATCTGAAGTTGTGTAGAGAGCTTAGTGATG	1137

## RESULT 6

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US-938-842A-4192
; Sequence 4192, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

```

QY 978 AAAAAAGTTTGAGGTTAAAGATAATTATAGTGGCTGAGATTTCTCCATTTCCGTAGCTTCT 1037  
|||||  
Db 781 AAAAAAGTTTGAGGTTAAAGATAATTATAGTGGCTGAGATTTCTCCATTTCCGTAGCTTCT 840  
|||||  
QY 1038 GGTCTCTTTTCTTTGTTTCATTGATCAAAAGCAAAATCACTTCTTCTTCTTCTTCTCTCG 1097  
|||||  
Db 841 GGTCTCTTTTCTTTGTTTCATTGATCAAAAGCAAAATCACTTCTTCTTCTTCTTCTCG 900  
|||||  
QY 1098 ATTTCTTACTGTTTCTTATCAACGAAATCTGGAAATTAATAATGGAATCTTTATCGAAT 1157  
|||||  
Db 901 ATTTCTTACTGTTTCTTATCAACGAAATCTGGAAATTAATAATGGAATCTTTATCGAAT 960  
|||||  
QY 1158 CCAAGCTGATTTGTTTCTTTCATTCAATCATCTCTCTAAAGTACTTAAAGATTGATTTA 1217  
|||||  
Db 961 CCAAGCTGATTTGTTTCTTTCATTCAATCATCTCTCTAAAGTACTTAAAGATTGATTTA 1020  
|||||  
QY 1218 TTGTGATGCTTCTTCTTATTTGTTGATGAATAACTTGAATCTGATCTTTTGTGTTTGTG 1277  
|||||  
Db 1021 TTGTGATGCTTCTTCTTATTTGTTGATGAATAACTTGAATCTGATCTTTTGTGTTG 1080  
|||||  
QY 1278 GATTAGTGGAAATTTTGTAAAGAGAAGATCTGAAGTTGTGTAGAGGAGCTTAGTG 1331  
|||||  
Db 1081 GATTAGTGGAAATTTTGTAAAGAGAAGATCTGAAGTTGTGTAGAGGAGCTTAGTG 1134  
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## RESULT 7

US-09-770-445-578/c  
; Sequence 578, Application US/09770445  
; Patent No. US20020023281A1

## GENERAL INFORMATION:

; APPLICANT: Gorlach, Jorn  
; APPLICANT: An, Yong-Qiang  
; APPLICANT: Hamilton, Carol M.  
; APPLICANT: Price, Jennifer L.  
; APPLICANT: Raines, Tracy M.  
; APPLICANT: Yu, Yang  
; APPLICANT: Rameaka, Joshua G.  
; APPLICANT: Page, Amy  
; APPLICANT: Matthew, Abraham V.  
; APPLICANT: Ledford, Brooke L.  
; APPLICANT: Woessner, Jeffrey P.  
; APPLICANT: Haas, William David  
; APPLICANT: Garcia, Carlos A.  
; APPLICANT: Krickler, Maja  
; APPLICANT: Slader, Ted  
; APPLICANT: Davis, Keith R.  
; APPLICANT: Allen, Keith  
; APPLICANT: Hoffman, Neil  
; APPLICANT: Hurban, Patrick  
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis  
; FILE REFERENCE: 2023US (PARA-012PRV)  
; CURRENT APPLICATION NUMBER: US/09/770,445  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: US 60/178,472  
; PRIOR FILING DATE: 2000-01-27  
; NUMBER OF SEQ ID NOS: 999  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 578  
; LENGTH: 865  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-770-445-578

Query Match 7.2%; Score 312.6; DB 9; Length 865;  
Best Local Similarity 95.8%; Pred. No. 3e-67;  
Matches 321; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 114 AGGAAATGTTTGTATCTGTTTTCAGGGAGGCTTTGTTTGAGAGGTCAAGAGCACATAC 173  
|||||  
Db 335 AAGAACCTGGTCTTCAAAACACAGAGGAGGCTTTGTTTGAGAGGTCAAGAGCACATAC 276  
|||||  
QY 174 AAGACATATTAGGGAGCAGCTGAATCAAGAGGAGGAAGAAAGAGCCCTTTTGTG 233  
|||||

Db 275 AAGACATATTAGGGAGCAGCTGAATCAAGAGGAGGAAGAAAGAGAGCCTTTTGTG 216  
|||||  
QY 234 AGCCCATTCATGAATTTGGAATGAAGGATATCAAAAGAACTTAACACAAAGGCCACGTCCT 293  
|||||  
Db 215 AGCCCATTCATGAATTTGGAATGAAGGATATCAAAAGAACTTAACACAAAGGCCACGTCCT 156  
|||||  
QY 294 TCCTTCAATCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 353  
|||||  
Db 155 TCCTTCAATCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 96  
|||||  
QY 354 GGTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 413  
|||||  
Db 95 GGTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 36  
|||||  
QY 414 TATATATGAGATGTTTGTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 448  
|||||  
Db 35 TATATATGAGATGTTTGTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1  
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## RESULT 8

US-09-770-961-961

; Sequence 961, Application US/09770961  
; Publication No. US20030115639A1

## GENERAL INFORMATION:

; APPLICANT: Gorlach, Jorn  
; APPLICANT: An, Yong-Qiang  
; APPLICANT: Hamilton, Carol M.  
; APPLICANT: Price, Jennifer L.  
; APPLICANT: Raines, Tracy M.  
; APPLICANT: Yu, Yang  
; APPLICANT: Rameaka, Joshua G.  
; APPLICANT: Page, Amy  
; APPLICANT: Matthew, Abraham V.  
; APPLICANT: Ledford, Brooke L.  
; APPLICANT: Woessner, Jeffrey P.  
; APPLICANT: Haas, William David  
; APPLICANT: Garcia, Carlos A.  
; APPLICANT: Krickler, Maja  
; APPLICANT: Slader, Ted  
; APPLICANT: Davis, Keith R.  
; APPLICANT: Allen, Keith  
; APPLICANT: Hoffman, Neil  
; APPLICANT: Hurban, Patrick  
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis  
; FILE REFERENCE: 2026 (PARA-015PRV)  
; CURRENT APPLICATION NUMBER: US/09/770,961  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 60/178,466  
; PRIOR FILING DATE: 2000-01-27  
; NUMBER OF SEQ ID NOS: 999  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 961  
; LENGTH: 479  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-770-961-961

Query Match 6.7%; Score 289; DB 11; Length 479;  
Best Local Similarity 73.8%; Pred. No. 1.6e-61;  
Matches 479; Conservative 0; Mismatches 0; Indels 170; Gaps 2;

QY 2241 ATAGCTATTTCTCTCCACGGCTAAGCGTAAACCAACAATCCTTTATCTCGAAAGAGC 2300  
|||||  
Db 1 ATAGCTATTTCTCTCTCCACGGCTAAGCGTAAACCAACAATCCTTTATCTCGAAAGAGC 60  
|||||  
QY 2301 GGAAGTGAACCATCTCTTATGTCAAAAACGGGTGTGAATGATGGAAGAGTCCCTTGA 2360  
|||||  
Db 61 GGAAGTGAACCATCTCTTATGTCAAAAACGGGTGTGAATGATGGAAGAGTCCCTTGA 120  
|||||  
QY 2361 TCAGAAAAGTGTGCGCATCTTGAGGTGATTTTTCATGGTGCATCTTTTTCAGTG 2420  
|||||

Db 121 TCAGAAAAAGTGTGCGATCCTG----- 142  
Qy 2421 TGTACATTGCTCTCATGTTATTAAATACAGATTGTGCTGCTGTTTATAGATGGCCAAAT 2480  
Db 143 -----AGATGGCCAAAT 153  
Qy 2481 GAAGATCGACAAACAATCAAAAGCTGAAGAGAAACCTCTCCAGAGAACAACTGTTTCAGAT 2540  
Db 154 GAAGATCGACAAACAATCAAAAGCTGAAGAGAAACCTCTCCAGAGAACAACTGTTTCAGAT 213  
Qy 2541 TGTTCACATCATCAGTATCTCTGCTGCTGATCCTCATCAATAAAGTTGTATAGAGACA 2600  
Db 214 TGTTCACATCATCAGTATCTCTGCTGCTGATCCTCATCAATAAAGTTGTATAGAGACA 273  
Qy 2601 TCAACGCGAAGCACTTTCGCGAGTTCTTTCGCTTTCACGGGAAGAGGTAAACAAACAACTT 2660  
Db 274 TCAACGCGAAGCACTTTCGCGAGTTCTTTCGCTTTCACGGGAAG----- 316  
Qy 2661 TCATTGCTATTGAGGTTTAAAGCAATAGTACTTTTCATGAACATAAACCGTGGGG 2720  
Db 317 ----- 316  
Qy 2721 AATAACAGGGAAGTACAGAAATACAGGGTAAGAAAGGACAACTCAGATTTGAATGCAA 2780  
Db 317 -----AGGAACTCAGAAATACAGGGTAAGAAAGGACAACTCAGATTTGAATGCAA 370  
Qy 2781 AATCTCTGAAAAACGGTAATAGCAAGGACCTCAGACTTTATCCGATGCATATCCCTGTGC 2840  
Db 371 AATCTCTGAAAAACGGTAATAGCAAGGACCTCAGACTTTATCCGATGCATATCCCTGTGC 430  
Qy 2841 TAGTCCATTGGGAGCTCAATAAACAAAGTTCTCTATCATCTCTCTC 2889  
Db 431 TAGTCCATTGGGAGCTCAATAAACAAAGTTCTCTATCATCTCTCTC 479

RESULT 9

US-09-934-455-119  
; Sequence 119, Application US/09934455  
; Publication No. US20030121070A1  
; GENERAL INFORMATION:  
; APPLICANT: Creelman, Robert  
; APPLICANT: Dubell, Arnold  
; APPLICANT: Heard, Jacqueline  
; APPLICANT: Jiang, Cai-Zhong  
; APPLICANT: Keddie, James  
; APPLICANT: Pilgrim, Marsha  
; APPLICANT: Ratcliffe, Oliver  
; APPLICANT: Reuber, Lynne  
; APPLICANT: Riechmann, Jose Luis  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Pineda, Omaisra  
; TITLE OF INVENTION: Genes for Modifying Plant Traits IV  
; FILE REFERENCE: MBI-0025  
; CURRENT APPLICATION NUMBER: US/09/934,455  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR FILING DATE: 2001-04-17  
; NUMBER OF SEQ ID NOS: 516  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 119  
; LENGTH: 2526  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (338)..(2275)  
; OTHER INFORMATION: G680  
US-09-934-455-119

Query Match 1.9%; Score 83.2; DB 11; Length 2526;  
Best Local Similarity 50.9%; Pred. No. 1.3e-09;  
Matches 233; Conservative 0; Mismatches 213; Indels 12; Gaps 1;

Qy 2847 CATGGGAGCTCAATAACAAGTTCTCTATCATCATCTCTTCCAGAGCCAGATGATCATC 2906  
Db 1137 CATCTGCTACTACTACAGCTTCTCATCAAGCGTTTCCAGCTTGTCTTACAGAGATGATT 1196  
Qy 2907 CCCACACAGTTCAGAGAGATTATAGTCTGTTTCTTAATCATATAATGTCAACCCCTTTTAC 2966  
Db 1197 ACCGTTCGTTCCTCCAGATATCATCTACTTTCTCCAATCTTATATGTCAACTCTCTAC 1256  
Qy 2967 AAACACCGGCTCTTTATATCTGCGGAACCTTTCGCTCATCATTTTGGCCCTCCCG----- 3020  
Db 1257 AGAATCTGCAGCTCATGCTGAGCTACATTGCTGCTTCGGTCTGGCTCTTATGCGAGTG 1316  
Qy 3021 -----ATTCTAGTGGTGGCTCACCTGTTTCCAGGAACTCACCTCCGAATCTGGCTGCCA 3074  
Db 1317 TCGGGAATTCGTGATTTCATCAACCCCAATGAGCTCTTCTCTCCCAAGTATAACTGCCA 1376  
Qy 3075 TGGCGCGAGCACTGTTGCGAGCTGCTAGTGTCTTGGTGGCTGCCAATGATTTACCTT 3134  
Db 1377 TTGCGCTGCTACAGTAGCTGCTGCAACTGCTTGGTGGCTTCTCATGGACTTCTTCTCTG 1436  
Qy 3135 TATGTGCTCTCTTAGTTAGTGGTGGTTCACCTAGTGTCTTCCATCTCTTGGAGCCAT 3194  
Db 1437 TATGGCTCCAGCTCAATAACATGTTTCCATCTTCAACTGTTGAGTTCCAACTCCAG 1496  
Qy 3195 CATGTGATGTAGAGTACACAAAGCAAGCACTTTTCAACATGTTCTGTGCGAGCCGAG 3254  
Db 1497 CAATGACTGAATGGATACCGTTTGAATACTCAACCGTTTGAGAAACAACACAGCTC 1556  
Qy 3255 ACCAAGAACACTCCGAGGATCAAAAGGCTCGATCTTTCA 3292  
Db 1557 TCGAAGATCAAAACCTTGGCTTCGAAATCTCCAGCTTCA 1594

RESULT 10

US-10-278-536-199  
; Sequence 199, Application US/10278536  
; Publication No. US20030131386A1  
; GENERAL INFORMATION:  
; APPLICANT: Samaha, Raymond  
; APPLICANT: Heard, Jacqueline  
; APPLICANT: Jiang, Cai-Zhong  
; APPLICANT: Pineda, Omaisra  
; APPLICANT: Reuber, Lynne  
; APPLICANT: Riechmann, Jose-Luis  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Keddie, James  
; APPLICANT: Ratcliffe, Oliver  
; APPLICANT: Pilgrim, Marsha  
; APPLICANT: Adam, Luc  
; APPLICANT: Broun, Pierre  
; TITLE OF INVENTION: STRESS-INDUCED POLYNUCLEOTIDES  
; FILE REFERENCE: MBI-011  
; CURRENT APPLICATION NUMBER: US/10/278,536  
; CURRENT FILING DATE: 2002-10-22  
; PRIOR APPLICATION NUMBER: 60/125,814  
; PRIOR FILING DATE: 1999-03-23  
; NUMBER OF SEQ ID NOS: 238  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 199  
; LENGTH: 2526  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; OTHER INFORMATION: G680  
US-10-278-536-199

Query Match 1.9%; Score 83.2; DB 15; Length 2526;  
Best Local Similarity 50.9%; Pred. No. 1.3e-09;



Matches	233;	Conservative	0;	Mismatches	213;	Indels	12;	Gaps	1;
QY	2847	CATTGGGAGCTCAATAACAAAGTTCTCTATCACATCTCTCTT	CAGAGCCAGATAGTCATC	2906					
Db	1137	CATCTGCTACTACTACAGTCTCTCATCAAGGTTTCCAGCTTGTCATT	CACAGGATGTT	1196					
QY	2907	CCACACAGTTGACAGGAGATTATCAGTCGTTTCTTAATCATATATATGTCAACCCCTTTTAC	2966						
Db	1197	ACCGTTCTGTTTCTCCAGANATCATCTACTTTCTCCAAATCTTATTATGTCAACTCTCTCTAC	1256						
QY	2967	AAACACCGGCTCTTTTATCTAGTCCCGCAACTTTTCGGCTCATCATTTTGGCTCTCCCG	3020						
Db	1257	AGAACTCTGCAGCTCATGCTGCAGCTACATTCGTGCTTGGTCTGGCTTATGCGAGTG	1316						
QY	3021	-----ATTCTAGTGGTGGCTCACTGTTTCAGGGAACACTCACTCCGAATCTGGCTGCCA	3074						
Db	1317	TCGGGAATTCGGTGATTTCATCAACCCCAATGAGCTCTTCCTCCCAAGTATAAATGCCA	1376						
QY	3075	TGGCGCGACCACTGTTGCAGCTGCTAGTGTCTGGTGGGTGCCAAATGGATATTATACCTT	3134						
Db	1377	TTGCGGTGCTACAGTAGCTGCTGCAACTGCTTGGTGGGCTTCTCATGACATCTTCTCGT	1436						
QY	3135	TATGTGCTCTCTTAGTTTCAGGTGGTTTCACTAGTGCATCTCTCAATCTACTTTTGGACCAT	3194						
Db	1437	TATCGGTCCAGCTCCAAATAACATGTGTTCATTTCTCAACTGTTTGCAGTTTCCAACTCCAG	1496						
QY	3195	CATGTGATGTAGAGTACACAAAAAGCAAGCACTTTTACAACATGGTTCTGTGCAGAGCCGAG	3254						
Db	1497	CAATGACTGAATGGATACCGTTGAAAATACTCAACCTGTTGAGAAAACAAACACAGCTC	1556						
QY	3255	AGCAAGAACTCCGAGGCATCAAGGCTCGATCTTCA	3292						
Db	1557	TGCAAGATCAAACTTGGCTTCGAAATCTCCAGGTTC	1594						

RESULT 11

US-09-938-842A-1116

Sequence 1116, Application US/09938842A

Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Krepis, Joel

APPLICANT: Wang, Xun

APPLICANT: Zhu, Tong

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE REFERENCE: SCRIPT300-3

CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2000-08-24

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/300,111

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 1116

LENGTH: 1938

TYPE: DNA

ORGANISM: Arabidopsis thaliana

US-09-938-842A-1116

	Query Match	1.9%	Score 81.6	DB 10	Length 1938
	Best Local Similarity	50.7%	pred. No. 2.8e-09		
	Matches 232	Conservative 0	Mismatches 214	Indels 12	Gaps 1
Qy	2847	CATTGGGGAGCTCAATAACAAAGTTCTCTATCACATCTCTTCAGAGCCAGATAGTCATC	2906		
Db	800	CATCTGCTACTACTACAGCTTCTCATCAAGCGTTTCCAGCTTGTTCATTCACAGGATGATT	859		
Qy	2907	CCACACAGATTGCAGGAGATTATCAGTTCGGTTTCTCTAATCATATATGTCACACCGCTTTTAC	2966		
Db	860	ACGGTTCGTTTCTCCAGATATCATCTACTTTCTTCCAAATCTTATTATGTCACATCTCTCTAC	919		

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RESULT 12
US-10-312-841-1
; Sequence 1, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeuten
; FILE REFERENCE: E01/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312,841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: chemically treated gel
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1

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Query Match	1.5%; Score 66.4; DB 12; Length 3673778;
Best Local Similarity	47.2%; Pred. No. 0.0031;
Matches 331; Conservative 0; Mismatches 366; Indels 5; Gaps 4;	
Qy	947 GTTCTCTTTGTAGCCTCGAAATAAATAAATTAAGAGTTTGGGTTAAAGATAATTATAG 1006
Db	56481 GATTTTGTTTTTTTTAGGTTTATTATGGTTAAAGAAATTTTAGTTTTCTGTTATTTTAA 56540
Qy	1007 TGGCTCGAGATTTCTCCATTTCCGTAGCTTCGTCTCTTTTCTT-TGTTTCAATCATCAA 1065
Db	56541 TTTTATATTTTTTATTTTTTGGATTATTTTTTATTTTTTTCTGAGGTAGTTATAGG 56600
Qy	1066 AAGCAAAATCACTTCTTCTTCTTCTCTCGAATTCCTACTGTTTCTTATCCAAACGAA 1125
Db	56601 TTTTGAAGATAATTGATGTTATAATTTGATTATATGCTTATAATGTAATATTAGTGAATAT 56660
Qy	1126 ATCTGAAATTAANAATGGAATCTTTATCGAATCCAGCTGATTTTGGTTCTCTTCATTGAA 1185
Db	56661 TTAATGTATGTGTGTGTTTTTTTAGGTATGGAGTTATTTTTGTAGTATATTTATTTTAA 56720
Qy	1186 TCATCTCTCTAAAGGTACTTAAAGATTGAATTTATTCGTATGGTCTTCTTATTTGGTATG 1245
Db	56721 TAATTTTTTATTTTTTGGAAATTTTAAAT-TAGTGAATGTGTTATTTTTTTTTTTTT 56779
Qy	1246 AATAAAGCTGACTTGATGTTTTTTCTTTTGTGGATTAGTGAAATTTTCTAAAGAGAAGAT 1305



; PRIOR APPLICATION NUMBER: DE 10043826.1					
; PRIOR FILING DATE: 2000-09-01					
; NUMBER OF SEQ ID NOS: 2424					
; SEQ ID NO 439					
; LENGTH: 15373					
; TYPE: DNA					
; ORGANISM: Artificial Sequence					
; FEATURE:					
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)					
US-10-311-455-439					
Query Match            1-48;   Score 62.4; DB 12; Length 15373;					
Best Local Similarity   46.5%; Pred. No. 0.00072;					
Matches 236; Conservative 0; Mismatches 271; Indels 1; Gaps 1;					
Qy	946	AGTTCTCTTTTGTAGCCTCGAAATAAATAATTAATAAGTTTGAGGTTAAAGATAATTATA	1005		
Db	6336	AGTTATATTAGTTATTGGATATAAAGAAGAAATATTATTTTTTTTGTTTTTTTAA	6395		
Qy	1006	GTCGCTCAGATTTCTCCATTTCCGTACTCTCTGGTCTCTTTCTCTTTCAITGATCAA	1065		
Db	6396	TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT	6455		
Qy	1066	AAGCAATCACTCTCTCTCTCTCTCGATTTCTTACTGTTTTCTTATCCAACGAA	1125		
Db	6456	TTTTTTTGGTTTTTTTAGAATTTTTTTTATTATTATTATTTTTTTTTTAGGTAAGTTT	6515		
Qy	1126	ATCTGGAATTAATAAGTAATCTTTATCGAATCCAAGCTGATTTTGTTCTTCATTGAA	1185		
Db	6516	ATATTATTTA	6574		
Qy	1186	TCATCTCTAAAGGTACTTAAGATTGATTTATTGTCATGCTCTTTCTTATTGTTGATG	1245		
Db	6575	TGTTGTTTTTTTTTAAGTTTTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	6634		
Qy	1246	AATAACTTGACTTGATTTGTTTTTTGTTGGAATTAGTGAATTTTGTAAAGAGAAGAT	1305		
Db	6635	TTTTTTTTTTTTTTTGAATTTTTTAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	6694		
Qy	1306	CTGAAGTTGTTAGAGGAGCTTAGTGATGAGACAATTCGTCGGAGAGATCTGGTTA	1365		
Db	6695	TTATTTTGTTTTTTTTTAGGAGATGTTATAATATTATAGTTTTTTTTTAGGATATAAATGA	6754		
Qy	1366	TTAAGGTAAATTAACTAAAATTTTAGGGGGAAGATGATTGTTTTAGGTGTCAAAGATTGAG	1425		
Db	6755	TTATTATTTTTTATTAAATTATTATTGAAAGAGATTATAAATTTAGGGTTTTAGTTTAA	6814		
Qy	1426	AATTTTAATGAACTTGATATAGACTCG	1453		
Db	6815	AAATTGTAATATATTCTAGTTGTTTCG	6842		
RESULT 15					
US-09-938-842A-2341					
; Sequence 2341, Application US/09938842A					
; Patent No. US20020160378A1					
GENERAL INFORMATION:					
; APPLICANT: Harper, Jeff					
; APPLICANT: Kreps, Joel					
; APPLICANT: wang, Xun					
; APPLICANT: Zhu, Tong					
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING					
; TITLE OF INVENTION: SAME, AND METHODS OF USE					
; FILE REFERENCE: SCRP1300-3					
; CURRENT APPLICATION NUMBER: US/09/938,842A					
; CURRENT FILING DATE: 2001-08-24					
; PRIOR APPLICATION NUMBER: US 60/227,866					
; PRIOR FILING DATE: 2000-08-24					
; PRIOR APPLICATION NUMBER: US 60/264,647					
; PRIOR FILING DATE: 2001-01-16					
; PRIOR APPLICATION NUMBER: US 60/300,111					
; PRIOR FILING DATE: 2001-06-22					
; NUMBER OF SEQ ID NOS: 5379					

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 24, 2003, 01:20:08 ; Search time 8553.69 Seconds  
(without alignments)  
12343.052 Million cell updates/sec

Title: US-10-084-553-1

Perfect score: 4344

Sequence: 1 Gcagtgggttcacttaacaga.....actcataagtaagcacaata 4344

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
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14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pin:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	735.2	16.9	740	28	AQ958316 LERAW81TF
C 2	430	9.9	430	9	AV809889
C 3	428	9.9	439	9	AV792310
C 4	425	9.8	426	9	AV804753

5	410.6	9.5	436	28	AQ958316
6	397.4	9.1	421	29	CC179314
7	397	9.1	421	29	CC179316
8	395.8	9.1	515	9	AA394931
C 9	393	9.0	393	9	AV814102
C 10	384	8.8	396	9	AV801368
C 11	366.4	8.4	393	28	AQ958317
C 12	360	8.3	360	9	AV784525
C 13	356.2	8.2	423	9	AV807633
C 14	339.4	7.8	580	9	AV827752
C 15	327.6	7.5	415	9	AV787515
C 16	320.6	7.4	415	9	AV811181
C 17	318.4	7.3	628	9	AV823536
C 18	315.6	7.3	403	9	AV799191
C 19	314.6	7.2	569	9	AV556228
C 20	306.6	7.1	396	9	AV545439
C 21	306.6	7.1	410	9	AV785900
C 22	306.6	7.1	415	9	AV803584
C 23	306.6	7.1	415	9	AV818664
C 24	306.6	7.1	418	9	AV799094
C 25	306.6	7.1	540	9	AV566656
C 26	306.6	7.1	685	9	AV784812
C 27	303.4	7.0	418	9	AV811618
C 28	302.6	7.0	391	9	AV797930
C 29	302.6	7.0	420	9	AV810366
C 30	302.6	7.0	577	9	AV534474
C 31	302	7.0	330	14	T03973
C 32	301.6	6.9	434	9	AV802892
C 33	299.6	6.9	422	9	AV816966
C 34	299.6	6.9	426	9	AV791925
C 35	298	6.9	422	9	AV819444
C 36	298	6.9	427	9	AV791998
C 37	298	6.9	436	9	AV819310
C 38	296.4	6.8	572	9	AV567367
C 39	296	6.8	296	9	AV565983
C 40	295.4	6.8	487	9	A1992931
C 41	283.6	6.5	438	9	AV520422
C 42	279.6	6.4	653	9	AV520014
C 43	278.6	6.4	605	9	AV520854
C 44	277.6	6.4	452	9	AV794212
C 45	269.2	6.2	403	9	AV787122

#### ALIGNMENTS

RESULT 1  
AQ958316/c  
LOCUS LERAW81TF LERA Arabidopsis thaliana genomic clone LERAW81, genomic survey sequence.  
DEFINITION  
ACCESSION AQ958316 GI:6786017  
VERSION AQ958316.1  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; euroids II; Brassicales; Brassicaceae; Arabidopsi.  
REFERENCE 1 (bases 1 to 740)  
AUTHORS Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T., Feldblum, T., Liang, F., Creasy, T. and Fraser, C.M.  
TITLE Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based polymorphisms  
JOURNAL Unpublished  
COMMENT Contact: Xiaoying Lin  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: at@tigr.org  
For additional information, see <http://www.tigr.org/tdb/at/at.html>

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Seq primer: TF
Class: Shotgun.
Location/Qualifiers
1..740
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Landsberg erecta"
/db_xref="taxon:3702"
/clone_lib="LERAW81"
/notes="Organ: Leaf; Vector: pHOS1; Total genomic DNA was sheared to 0.9-1 Kbp before ligation."
BASE COUNT      184 a   176 c   178 g   202 t
ORIGIN
Query Match      16.9%; Score 735.2; DB 28; Length 740;
Best Local Similarity 99.6%; Pred. No. 3.2e-107;
Matches 737; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2887 TTCAGAGCCAGATAGTATCCCAACACAGTTGCAGGAGATTATCAGTCGTTTCTTAATCA 2946
DB 740 TTCAGAGCCAGATAGTATCCCAACACAGTTGCAGGAGATTATCAGTCGTTTCTTAATCA 681
QY 2947 TATAATGTCAACCCCTTTTACAAACACCGGCTCTTTTATCTGCGCAACTTTCGCTCATC 3006
DB 680 TATAATGTCAACCCCTTTTACAAACACCGGCTCTTTTATCTGCGCAACTTTCGCTCATC 621
QY 3007 ATTTGGCCCTCCCGATTTAGTGTGGCTCACCTGTTCCAGGGAACCTCACTCCGAATCT 3066
DB 620 ATTTGGCCCTCCCGATTTAGTGTGGCTCACCTGTTCCAGGGAACCTCACTCCGAATCT 561
QY 3067 GGCTGCCATGGCCGACGCACTGTTGAGCTGCTAGTGTGTTGGTGGCTGCCAATGGATT 3126
DB 560 GGCTGCCATGGCCGACGCACTGTTGAGCTGCTAGTGTGTTGGTGGCTGCCAATGGATT 501
QY 3127 ATTACCTTTATGTCTCTCTTAGTTCAGGTGTTTCACTAGTCACTCTCCATCTACTTT 3186
DB 500 GTTACCTTTATGTCTCTCTTAGTTCAGGTGTTTCACTAGTCACTCTCCATCTACTTT 441
QY 3187 TGGACCATCATGTGATGTAGGTACACAAAGCAAGCACTTTCAACATGGTTCTGTGCA 3246
DB 440 TGGACCATCATGTGATGTAGGTACACAAAGCAAGCACTTTCAACATGGTTCTGTGCA 381
QY 3247 GAGCCGAGACGAAGAACTCCGAGGATCAAGGCTCGATCTTCACTGGACTCAGAGGA 3306
DB 380 GAGCCGAGACGAAGAACTCCGAGGATCAAGGCTCGATCTTCACTGGACTCAGAGGA 321
QY 3307 TGTGAAATTAAGAGTAACACAGTTTGTCTATGAGCAGCCTTCTGCAACACCTCGAGGTGA 3366
DB 320 TGTGAAATTAAGAGTAACACAGTTTGTCTATGAGCAGCCTTCTGCAACACCTCGAGGTGA 261
QY 3367 TGCAAGGGTTTCAGATCGAGCAGAGACAGAAACAAAGTTGACCGTCTCTCGTGTGCTC 3426
DB 260 TGCAAGGGTTTCAGATCGAGCAGAGACAGAAACAAAGTTGACCGTCTCTCGTGTGCTC 201
QY 3427 AATACCTCCGCTGAGTGTATGATGTTGAGGCGGATGCATCAGAAAGGCAAGAGATGG 3486
DB 200 AATACCTCCGCTGAGTGTATGATGTTGAGGCGGATGCATCAGAAAGGCAAGAGATGG 141
QY 3487 CACCAATGGTGGAGTGAAGAAACGAATGAAGACACTAATAAACCCTCAAACTTCAGAGTC 3546
DB 140 CTCCAATGGTGGAGTGAAGAAACGAATGAAGACACTAATAAACCCTCAAACTTCAGAGTC 81
QY 3547 CAATGACGCGGAGTGAATCAGTCCCAATATAACCGATCCATGGAAGTCTGTGTCTGA 3606
DB 80 CAATGACGCGGAGTGAATCAGTCCCAATATAACCGATCCATGGAAGTCTGTGTCTGA 21
QY 3607 CGAGGTACTTACTTGGACTA 3626
DB 20 CGAGGTACTTACTTGGAGTA 1
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/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL09-61-K22"
/dev_stage="plants at various developmental stages from germination to mature seeds"
/lab_host="DH10B"
/clone_lib="RAFL9"
/notes="Site 1: BamHI; Site 2: SalI; subjected to dehydration (1, 2, 5, 10, 24 hr) treatments"
BASE COUNT      143 a   80 c   78 g   129 t
ORIGIN
Query Match      9.9%; Score 430; DB 9; Length 430;
Best Local Similarity 100.0%; Pred. No. 1.5e-58;
Matches 430; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 TTACAAGAACCTGGTCTTCAAAACGACAGAGTTAAACCAATCTCTTTAACTCTGTGT 72
DB 430 TTACAAGAACCTGGTCTTCAAAACGACAGAGTTAAACCAATCTCTTTAACTCTGTGT 371
QY 73 TGTGTCATCTAATCTAGAAATGGAAGCTCAAAATCTCGAGGAATTTGTTTATCT 132
DB 370 TGTGTCATCTAATCTAGAAATGGAAGCTCAAAATCTCGAGGAATTTGTTTATCT 311
QY 133 GTTTCAGGAGGCTTTGTTTGAAGGTCGAAGACACATACAAAGACATATTAGGGAGCA 192
DB 310 GTTTCAGGAGGCTTTGTTTGAAGGTCGAAGACACATACAAAGACATATTAGGGAGCA 251
QY 193 GCTGAATCAAGGAGGAAGAAAGAGAGAGCCCTTTTGGGCCATTTCATGAATTTGA 252
DB 250 GCTGAATCAAGGAGGAAGAAAGAGAGAGCCCTTTTGGGCCATTTCATGAATTTGA 191
QY 253 ATGAAGGATATCAAAAGAAATCTTAACCAAGGCCACGTCCTTCTCAATCTTCTTCT 312
DB 190 ATGAAGGATATCAAAAGAAATCTTAACCAAGGCCACGTCCTTCTCAATCTTCTTCT 131
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## ORIGIN

Query Match 9.8%; Score 425; DB 9; Length 426;  
Best Local Similarity 100.0%; Pred. No. 9.1e-58;  
Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3783 AGATATCAATGGCACTTGATCTCTTAACCTTCACAGCTCAGTTAAACACCAAGTTGATGATCAA 3842  
Db |||||  
Qy 426 AGATATCAATGGCACTTGATCTCTTAACCTTCACAGCTCAGTTAAACACCAAGTTGATGATCAA 367  
Db |||||  
Qy 3843 GAGGAGAGAGAAACACAGGATTTCTTGGATTCGATAGATGCTTCAAGCTAATGAGT 3902  
Db |||||  
Qy 366 GAGGAGAGAGAAACACAGGATTTCTTGGATTCGATAGATGCTTCAAGCTAATGAGT 307  
Db |||||  
Qy 3903 AGAGGAGAGAAACAGGTTTAAACCATACAAAAGATGTTCCATGGAAGCCAAAGAAAGTAGA 3962  
Db |||||  
Qy 306 AGAGGAGAGAAACAGGTTTAAACCATACAAAAGATGTTCCATGGAAGCCAAAGAAAGTAGA 247  
Db |||||  
Qy 3963 ATCTCAACAAATCTCATCTCATCTGATGGAACAGAAAGATCCCAACCGATCGGTTG 4022  
Db |||||  
Qy 246 ATCTCAACAAATCTCATCTCATCTGATGGAACAGAAAGATCCCAACCGATCGGTTG 187  
Db |||||  
Qy 4023 GAAACTCAAGCTTCCACATGAGACTTATTTTCTATCTGATCTGTTGTTGACTCTGTTT 4082  
Db |||||  
Qy 186 GAAACTCAAGCTTCCACATGAGACTTATTTTCTATCTGATCTGTTGTTGACTCTGTTT 127  
Db |||||  
Qy 4083 TTAAGTTTTCAAGACCACTGCTACATTTTCTTTTCTTTGAGGCTTTGTTATTTGTTTC 4142  
Db |||||  
Qy 126 TTAAGTTTTCAAGACCACTGCTACATTTTCTTTTCTTTGAGGCTTTGTTATTTGTTTC 67  
Db |||||  
Qy 4143 CTGTCATAGCTTCTCTGTAACATTTGACTCTGTATTTATTTCAACAAATCAAACTGTT 4202  
Db |||||  
Qy 66 CTGTCATAGCTTCTCTGTAACATTTGACTCTGTATTTATTTCAACAAATCAAACTGTT 7  
Db |||||  
Qy 4203 TAATC 4207  
Db |||||  
Qy 6 TAATC 2

## RESULT 5

LOCUS AQ969326  
DEFINITION LERJMI0TR LERG Arabidopsis thaliana genomic clone LERJMI0, genomic survey sequence.  
ACCESSION AQ969326  
VERSION AQ969326.1 GI:6797027  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
; euroids II; Brassicales; Brassicaceae; Arabidopsi.  
REFERENCE 1 (bases 1 to 436)  
AUTHORS Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T., Feldblum, T., Liang, F., Creasy, T. and Fraser, C.M.  
TITLE Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based polymorphisms  
JOURNAL Unpublished  
COMMENT Contact: Xiaoying Lin  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: at@tigr.org  
For additional information, see <http://www.tigr.org/tdb/at/at.html>  
Seq primer: TR  
Class: shotgun.  
Location/Qualifiers  
1. .436  
/organism="Arabidopsis thaliana"  
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/strain="Landsberg erecta"

## FEATURES

## source

1. .436  
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/clone="LERJMI0"

/clone\_lib="LERG"

/note="Organ: Leaf; Vector: pUC19JK; Total genomic DNA was sheared to 0.4-0.7 Kbp before ligation."

## BASE COUNT

138 a 78 c 99 g 121 t

Query Match 9.5%; Score 410.6; DB 28; Length 436;

Best Local Similarity 97.7%; Pred. No. 1.8e-55;

Matches 427; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

Qy 518 AATAACGATATGGCCCTTATGCTAAAGAAACAAACCTTATGGGTCTAAAAAATAAGC 577  
Db |||||  
Qy 1 ATTAACGATATGGCCCTTATGCTAAAGAAACAAACCTTATGGGTCTAAAAAATAAGC 60  
Db |||||  
Qy 578 CCAATATAAATAGTATGCCCAATAAAGTTTAGGTCCATTTAGAGTGTGAGAAATAGCGGTG 637  
Db |||||  
Qy 61 CCAATATAAATAGTATGCCCAATAAAGTTTAGGTCCATTTAGAGTGTGAGAAATAGCGGTG 119  
Db |||||  
Qy 638 TAGTGAACCGCAGAGAAATGCGCTTCGATTTGTTGGTGAAGTGTGCTAGATTCCCGG 697  
Db |||||  
Qy 120 TAGTGAACCGCAGAGAAATGCGCTTCGATTTGTTGGTGAAGTGTGCTAGATTCCCGG 179  
Db |||||  
Qy 698 GTCCACTCATGTTTCTAGTGTATCAGACACGCTGTGCAAACTGGTGGAGAGATTAACG 757  
Db |||||  
Qy 180 GTCCACTCATGTTTCTAGTGTATCAGACACGCTGTGCAAACTGGTGGAGAGATTAACG 239  
Db |||||  
Qy 758 ATCTTAAGTAGTCCCACTAGATCAAGATATTTAAGCAATTTGACCTTTTAACTTTTCA 817  
Db |||||  
Qy 240 ATCTTAAGTAGTCCCACTAGATCAAGATATTTAAGCAATTTGACCTTTTAACTTTTCA 299  
Db |||||  
Qy 818 GGTAGTCCCGAACTCGTGGCTTAGAATACAAAGAGTTGTGAACAGTTGATGTTAAG 877  
Db |||||  
Qy 300 GGTAGTCCCGAACTCGTGGCTTAGAATACAAAGAGTTGTGAACAGTTGATGTTAAG 359  
Db |||||  
Qy 878 ATGGACAAGAAATGTAACTTGAACAAAAGCTGAATCATCTCTTACGCCACTAGTATGTTGA 937  
Db |||||  
Qy 360 ATGGACAAGAAATGTAACTTGAACAAAAGCTGTATCATCTCTTACGCCACTAGTATGTTGA 419  
Db |||||  
Qy 938 CATATGCCAGTTTCTTT 954  
Db |||||  
Qy 420 CATATGCCAGTTTCTTT 436  
Db |||||

## RESULT 6

LOCUS CCI179314  
DEFINITION SALK\_067774.47.95.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK\_067774.47.95.x, genomic survey sequence.  
ACCESSION CCI179314  
VERSION CCI179314.1 GI:30317865  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
; euroids II; Brassicales; Brassicaceae; Arabidopsi.  
REFERENCE 1 (bases 1 to 421)  
AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.  
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  
JOURNAL Unpublished  
COMMENT Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

Location/Qualifiers

## FEATURES

source

1..421

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SALK\_067774.47.95.x"

/note="PCR was performed on Arabidopsis thaliana TDNA insertion lines"

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)

136 a 44 c 91 g 150 t

## BASE COUNT

ORIGIN

Query Match

Best Local Similarity 98.1%; Pred. No. 2.3e-53; Length 421;

Matches 413; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

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QY 1162 GCTGATTTTGTCTTCTTCAATCAATCATCTCTAAAGTACTTAAGATTGATTATTGT 1221

Db 61 GCTGATTTTGTCTTCTTCAATCAATCATCTCTAAAGTACTTAAGATTGATTATTGT 120

QY 1222 CATGCTCTTTCTTATTTGTTGATGAATACTTGACTTGATTGTTTGTGTTTGTGGATT 1281

Db 121 CATGCTCTTTCTTATTTGTTGATGAATACTTGACTTGATTGTTTGTGTTTGTGGATT 180

QY 1282 AGTGAATTTTCTAAAGGAAGATCTGAAGTTGTGTAGAGAGCTTTAGTGATGGAGACAA 1341

Db 181 AGTGAATTTTCTAAAGGAAGATCTGAAGTTGTGTAGAGAGCTTTAGTGATGGAGACAA 240

QY 1342 ATTCGCTCGGAGAAATCTGTTTATTAAAGTAAATTA--CTAAATTTTAGGGGGAAGAT 1399

Db 241 ATTCGCTCGGAGAAATCTGTTTATTAAAGTAAATTA--CTAAATTTTAGGGGGAAGAT 300

QY 1400 GATTGTTTATAGTGTCAAAGATTGAGAATTTTAATGAACTTTGATATAGACTCGGAAGCC 1459

Db 301 GATTGTTTATAGTGTCAAAGATTGAGAATTTTAATGAACTTTGATATAGACTCGGAAGCC 360

QY 1460 ATATACGATTAACAAAGCAACGTGAAGGTGGACTGAGGAAGAACATAATAGATTCAATGA 1519

Db 361 ATATACGATTAACAAAGCAACGTGAAGGTGGACTGAGGAAGAACATAATAGATTCAATGA 420

QY 1520 A 1520

Db 421 A 421

## RESULT 7

CC179316

LOCUS

DEFINITION SALK\_067780.51.35.x Arabidopsis thaliana TDNA insertion lines

Arabidopsis thaliana genomic clone SALK\_067780.51.35.x, genomic

survey sequence.

CC179316

VERSION CC179316.1 GI:30317867

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 421)

REFERENCE

AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab

,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.

, Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA.

Class: TDNA tagged.

Location/Qualifiers

1..421

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SALK\_067780.51.35.x"

/note="PCR was performed on Arabidopsis thaliana TDNA insertion lines"

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)

135 a 44 c 92 g 150 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 99.5%; Pred. No. 2.6e-53; Length 421;

Matches 419; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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Db 1 CTTACTGTTTCTTATCCCAACGAAATCTGGAATTAATAATGGAATCTTTATCGAATCCAA 60

QY 1162 GCTGATTTTGTCTTCTTCAATCAATCATCTCTAAAGTACTTAAGATTGATTATTGT 1220

Db 61 GCTGATTTTGTCTTCTTCAATCAATCATCTCTAAAGTACTTAAGATTGATTATTGT 120

QY 1221 TCATCGTCTTCTTCTTCAATCAATCATCTCTAAAGTACTTAAGATTGATTATTGT 1280

Db 121 TCATCGTCTTCTTCTTCAATCAATCATCTCTAAAGTACTTAAGATTGATTATTGT 180

QY 1281 TAGTGGAAATTTTGTAAAGAGAGATCTGAAAGTTGTGTAGAGAGCTTAGTGATGGAGACA 1340

Db 181 TAGTGGAAATTTTGTAAAGAGAGATCTGAAAGTTGTGTAGAGAGCTTAGTGATGGAGACA 240

QY 1341 AATTCGTCGGAGAGATCTGGTTATTAAAGTAAATTTAGGGGGAAGAT 1399

Db 241 AATTCGTCGGAGAGATCTGGTTATTAAAGTAAATTTAGGGGGAAGAT 300

QY 1400 GATTGTTTATAGTGTCAAAGATTGAGAATTTTAATGAACTTTGATATAGACTCGGAAGCC 1459

Db 301 GATTGTTTATAGTGTCAAAGATTGAGAATTTTAATGAACTTTGATATAGACTCGGAAGCC 360

QY 1460 ATATACGATTAACAAAGCAACGTGAAGGTGGACTGAGGAAGAACATAATAGATTCAATGA 1519

Db 361 ATATACGATTAACAAAGCAACGTGAAGGTGGACTGAGGAAGAACATAATAGATTCAATGA 420

QY 1520 A 1520

Db 421 A 421

## RESULT 8

AA394931

LOCUS

DEFINITION

26812 Lambda-PRL2 Arabidopsis thaliana cDNA clone 109K9XP 3', mRNA

AA394931

LOCUS

DEFINITION

26812 Lambda-PRL2 Arabidopsis thaliana cDNA clone 109K9XP 3', mRNA

AA394931

LOCUS

DEFINITION

26812 Lambda-PRL2 Arabidopsis thaliana cDNA clone 109K9XP 3', mRNA

[illegible]

Qy	3935	ATGTTCCATGGAGGCCAAAGAAAGTGAAGA	CCTCAACAAACAATCCTATCATTCATGTGGA	3994
Db	273	ATGTTCCATGGAGGCCAAAGAAAGTGAAGA	CCTCAACAAACAATCCTATCATTCATGTGGA	214
Qy	3995	ACAGAAAGATCCCAAAACCGATGCGGTTGG	AAACTCCAAGCTTCCACATGAGACTCTATTTT	4054
Db	213	ACAGAAAGATCCCAAAACCGATGCGGTTGG	AAACTCCAAGCTTCCACATGAGACTCTATTTT	154
Qy	4055	CATCTGATCTGTTGTTTTGTGTA	CTCTGTTTTTAAAGTTTTCAAGACCACATGCTACATTTCCT	4114
Db	153	CATCTGATCTGTTGTTTTGTGTA	CTCTGTTTTTAAAGTTTTCAAGACCACATGCTACATTTCCT	94
Qy	4115	TTTCTTTTGAGGCCTTTGTATTTGTTTCC	TGCTGCATAGTCTTCTCTGTAACATTTGACTC	4174
Db	93	TTTCTTTTGAGGCCTTTGTATTTGTTTCC	TGCTGCATAGTCTTCTCTGTAACATTTGACTC	34
Qy	4175	TGTAATTATCAACAATCATAAAC	GTTTTAATC 4207	
Db	33	TGTAATTATCAACAATCATAAAC	GTTTTAATC 1	

RESULT 10				
AV801368/c				
LOCUS	AV801368	396 bp	mRNA	linear EST 29-MAR-2002
DEFINITION	AV801368	RAFL9	Arabidopsis thaliana	CDNA clone RAFL09-27-N02 3', mRNA sequence.

ACCESSION	AV801368
VERSION	AV801368.1
KEYWORDS	GI:19835353
SOURCE	EST
ORGANISM	Arabisopsis thaliana (thale cress)
REFERENCE	Arabisopsis thaliana
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eutrosids II; Brassicales; Brassicaceae; Arabidopsids.
TITLE	1 (bases 1 to 396)
	Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shingawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.
	Large scale analysis of Arabidopsis full-length cDNA (2002b)

Unpublished  
JOURNAL  
COMMENT

Contact: Motoaki Seki  
Plant Functional Genomics Research Group  
RIKEN Genomic Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-4359  
Fax: 81-298-36-9060  
Email: msek@rtc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda E1C-1 vector (Carinci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further details.

FEATURES	Location/Qualifiers
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	/dev_stage="plants at various developmental stages from germination to mature seeds"
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	/notes="Site 1: BamHI; Site 2: SalI; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24 hr) treatments"
BASE COUNT	133 a 68 c 74 g 121 t

Query Match 8.8%; Score 384; DB 9; Length 396;

Best Local Similarity    99.7%;    Pred. No. 3.1e-51;					
Matches 395; Conservative    0; Mismatches    0; Indels    1; Gaps    1;					
QY	3823	TAAACACAGTTGATGATCAAGAGAGAGAAGACAACACAGGATTCTTGGAAATCGGATTAG	3882		
Db	396	TAAACACAGTTGATGATCAAGAGAGAGAAGACAACACAGGATTCTTGGAAATCGGATTAG	337		
QY	3883	ATGCTTCAAAGCTAATGAGTAGGAAGAAACAGGTTTTTAAACCATACAAAAGATGTTCCA	3942		
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QY	4003	ATCCCAAACGGATGCGGTTCGGAACACTCAAGCTTCCACATGAGACTCTATTATTTTCATCTGAT	4062		
Db	216	ATCCCAAACGGATGCGGTTCGGAACACTCAAGCTTCCACATGAGACTCTATTATTTTCATCTGAT	157		
QY	4063	CTGTTGTTTGCTACTCTGTTTTTAAGTTTTCAAGACACACTGCTACATTTTCTTTTTCTTTT	4122		
Db	156	CTGTTGTTTGCTACTCTGTTTTTAAGTTTTCAAGACACACTGCTACATTTTCTTTTTCTTTT	98		
QY	4123	GAGSCCTTTGTATTGTTTCTCTTGTGCATAGTCTTCTCTGTAACATTGACTCTGTATTAT	4182		
Db	97	GAGSCCTTTGTATTGTTTCTCTTGTGCATAGTCTTCTCTGTAACATTGACTCTGTATTAT	38		
QY	4183	TCAACAAATCATAAACGTGTTTAATCTTTTTTTTTTCC	4218		
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RESULT 11	393 bp	DNA	linear	GSS 28-JAN-2000
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ACCESSION	AF058317			
VERSION	AF058317.1			
KEYWORDS	GI:6786018			
SOURCE	GSS.			
ORGANISM	Arabidopsis thaliana (thale cress)			
	Arabidopsis thaliana			

REFERENCE  
1 (bases 1 to 393)  
AUTHORS  
Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T.,  
Feldblyum, T., Liang, F., Creasy, T. and Fraser, C.M.  
TITLE  
Genomic survey sequencing of *Landsberg erecta* ecotype of  
*Arabidopsis thaliana* and identification of sequence-based  
polymorphisms  
JOURNAL  
Unpublished  
CONTACT  
Contact: Xiaoying Lin  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: at@tigr.org  
For additional information, see <http://www.tigr.org/tdb/at/at.html>  
Seq primer: TR  
Class: shotgun.

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393    ...
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 QY 2826 TGCATATCCCTGTGCTAGTGGGAGCTCAATAAAGTTCCTATCACATCCTC 2885  
 DB 73 TGCATATCCCTGTGCTAGTGGGAGCTCAATAAAGTTCCTATCACATCCTC 132  
 QY 2886 CTTGAGAGCAGATAGTATATCCCAACAGTTCGAGGAGTATATCAGTCGTTTCTTAATC 2945  
 DB 133 CTTGAGAGCAGATAGTATATCCCAACAGTTCGAGGAGTATATCAGTCGTTTCTTAATC 192  
 QY 2946 ATATAATGTCAACCTCTTACAAACCGGCTCTTATCTGCGGCACTTTCGCTCAT 3005  
 DB 193 ATATAATGTCAACCTCTTACAAACCGGCTCTTATCTGCGGCACTTTCGCTCAT 252  
 QY 3006 CATTTTGGCCTCCGATTTCTAGTGGTGGCTCACCTGTTCCAGGGAACCTCACCTCCGAATC 3065  
 DB 253 CATTTTGGCCTCCGATTTCTAGTGGTGGCTCACCTGTTCCAGGGAACCTCACCTCCGAATC 312  
 QY 3066 TGGCTGCCATGGCGGCGACCACTGTTGAGCTGCTAGTGTGTTGGGCTGCCAATGGAT 3125  
 DB 313 TGGCTGCCATGGCGGCGACCACTGTTGAGCTGCTAGTGTGTTGGGCTGCCAATGGAT 372  
 QY 3126 TATTACCTTTATGTGC 3141  
 DB 373 TGGTACCTTTATGGGC 388

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 LOCUS AV784525 360 bp mRNA linear EST 28-MAR-2002  
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 mRNA sequence.  
 ACCESSION AV784525  
 VERSION AV784525.1 GI:19803315  
 KEYWORDS EST.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
 ; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 REFERENCE 1 (bases 1 to 360)  
 AUTHORS Seki.M., Narusaka.M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,  
 Oono.Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,  
 Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.  
 and Shinozaki,K.  
 Large scale analysis of Arabidopsis full-length cDNA (2002b)  
 Unpublished  
 Contact: Motoaki Seki  
 Plant Functional Genomics Research Group  
 RIKEN Genomic Sciences Center  
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
 Tel: 81-298-36-4359  
 Fax: 81-298-36-9060  
 Email: msekic@rcc.riken.go.jp  
 An Arabidopsis full-length cDNA library was constructed essentially  
 as reported previously (Seki et al., 1998). This clone is in a  
 modified pBluescript vector as a SstI/XhoI insert. Please visit our  
 web site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for  
 further details.

TITLE Location/Qualifiers  
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/lab\_host="SOLR"  
 /clone\_lib="RAFL5"  
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 BASE COUNT 128 a 59 c 69 g 104 t  
 ORIGIN

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 Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 3919 TTAACCATACAAAGATGTTCCATGGAAGCAAGAAAGTAGAATCTCAACAACATC 3978  
 DB 300 TTAACCATACAAAGATGTTCCATGGAAGCAAGAAAGTAGAATCTCAACAACATC 241  
 QY 3979 CTATCATTCATGTGGAACAGAAAGATCCCAACGGATCGGTTGGAACCTCAAGCTTCCA 4038  
 DB 240 CTATCATTCATGTGGAACAGAAAGATCCCAACGGATCGGTTGGAACCTCAAGCTTCCA 181  
 QY 4039 CATGAGACTCTATTTTCATCTGATCTGTTGTGACTCTGTTTAAAGTTTCAAGACC 4098  
 DB 180 CATGAGACTCTATTTTCATCTGATCTGTTGTGACTCTGTTTAAAGTTTCAAGACC 121  
 QY 4099 ACTGCTACATTTCTTTTCTTTTGGCCCTTTGATTTGTTCTTCTGTCATAGTCTTC 4158  
 DB 120 ACTGCTACATTTCTTTTCTTTTGGCCCTTTGATTTGTTCTTCTGTCATAGTCTTC 61  
 QY 4159 CTGTAACATTTGACTCTGTATTATTCAACAAATCATAAATCTTTTAACTTTTTTTTCC 4218  
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RESULT 13  
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 mRNA sequence.  
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 VERSION AV807633.1 GI:19841618  
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 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
 ; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 REFERENCE 1 (bases 1 to 423)  
 AUTHORS Seki.M., Narusaka.M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,  
 Oono.Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,  
 Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.  
 and Shinozaki,K.  
 Large scale analysis of Arabidopsis full-length cDNA (2002b)  
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 Contact: Motoaki Seki  
 Plant Functional Genomics Research Group  
 RIKEN Genomic Sciences Center  
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
 Tel: 81-298-36-4359  
 Fax: 81-298-36-9060  
 Email: msekic@rcc.riken.go.jp  
 An Arabidopsis full-length cDNA library was constructed essentially  
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 and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et  
 al., submitted for publication) digested with BamHI and SalI. This  
 clone is in a modified pBluescript vector. Please visit our web  
 site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further  
 details.

TITLE Location/Qualifiers  
 JOURNAL 1. .423  
 COMMENT /organism="Arabidopsis thaliana"

FEATURES  
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Gaps	4;						
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Qy	3855	AACACAGGATTTCTTTGGAATCGGATTAGATGCTTCAAAGCTTAATGAGTAGAGGAAGAACA	3914				
Db	364	AACACAGGATTTCTTTGGAATCGGATTAGATGCTTCAAAGCTTAATGATTAGA-GAAGCACA	306				
Qy	3915	GGTTTTAAACCATACAAAGAGATGTTTCATGGAAGCCAAAGAAAGCTAGAACTCTCAACAAC	3974				
Db	305	GGTTTTAAACCATACAAAGAGATGTTCCAT-GAACCCCAAGAAAGTAGATCTCTCGACAC	247				
Qy	3975	AATCCTATCATTTGATGGAACAGAAAGATCCCAACGGATGCGGTTGGAAACTCAAGCT	4034				
Db	246	CATCCTATCATTTGATGGAACAGAAAGATCCCAACGGATGCGGTTGGAAACTCAAGCT	187				
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Db	186	TCCACATGAGACTCTATTTTTCATCTGATCTGTTGTTGTACTCTGTTTTTAAAGTTTTCAA	127				
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Qy	4155	CTTCCTGTAACATTTTGACTCTGTAATTATTCAAACAAATCATAAA-CTGTTTAAATCTTTTT	4213				
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Db	6	TTTCC 2					

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LOCUS	AV827752 580 bp mRNA linear EST 01-APR-2002
DEFINITION	AV827752 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-19-A10 5',

Accession	AV827752
Version	AV827752.1
Keywords	EST
Source	Arabidopsis thaliana (thale cress)
Organism	Arabidopsis thaliana
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Eurosid II; Brassicales; Brassicaceae; Arabidopsids.

**REFERENCE**

**AUTHORS**

Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakaajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ichii,Y., Arakawa,T., Shibata,K., Shingawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.

**TITLE**

Large scale analysis of Arabidopsis full-length cDNA (2002b)

Unpublished  
Contact: Motoaki Seki  
Plant Functional Genomics Research Group  
RIKEN Genomic Sciences Center

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-4359  
Fax: 81-298-36-9060  
Email: mseki@etc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified Bluescript vector. Please visit our web site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further details.

FEATURES	Location/Qualifiers
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	/clone_lib="RAFL9"
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Qy	1501	AACATAATAGATTCAITTGAGGCTTTTCAGGCTTTATCGTAGAGCATTGCACAGAACTTGAAG	1560		
Db	168	AACATAATAGATTCAITTGAGGCTTTTCAGGCTTTATCGTAGAGCATTGCACAGAACTTGA--	225		
Qy	1561	GTTGATTTTTATTTCGCCITTTATATGTCATTATTTTTGTGTGTCAGAGGTTTGTCTTCAA	1620		
Db	226	-----	225		

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Db	226	-----AGAACATGTAGCAACAAAAA	CTGCTGCCAGATA	259
Qy	1681	AGAAGTCACGCTCAGAAAATTTTTCTCCAAGGTAAAA	TCGGTTAAATTTTGAATGATGTTTC	1740
Db	260	AGAAGTCACGCTCAGAAAATTTTTCTCCAAGGTAAAA	TCGGTTAAATTTTGAATGATGTTTC	319

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Db	320	TCACTTCATTGGCTTAATGCTTTAAGACTTATTGAAGCCAGCAGTTCCTTGCTTCCTT	379

Qy	1801	TTGCTTCTTAGTCAGGAGATAGATAGATTACGTTTTAGAGTTTGTAGTAATGAGCAATAA 1859
Db	380	TTGCTTCTTAGTCAGGAGATAGATAGATTACCGTTTTAGAGTTTGTAGTAATGAGCAATAA 439

1919	GTCTTAAATAGTGTGGAGAAATGACGAGATGTAATCGTTTCTTTTGGTTATGCGCTATAT	1919
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Qy		
440	GTCTTAAATAGTGTGGAGAAATGACGAGATGTAATCGTTTCTTTTGGTTATGCGCTATAT	499
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1920	CTTGTTTAATCCAAACATGTACATAGATCTTTCAGAAGAACTGTTAGTTTCTTTTACGATTC	1979
Qy		

Db 500 CTTGTT-ATCCACAAACATGTACATAGATTCTT NAGAGANTGTTAGTCCCTTTAGATTC 558  
 Qy 180 TTCAGATAAACTTGTGTCCTTCT 2001

Db 559 TTCAGATAAACTAGCGTCTTCT 580

RESULT 15

RESULT 15



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mRNA sequence.  
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VERSION AV787515.1 GI:19806305  
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ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
REFERENCE 1 (bases 1 to 415)  
AUTHORS Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,  
Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,  
Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.  
and Shinozaki,K.  
TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)  
JOURNAL Unpublished  
COMMENT Contact: Motoaki Seki  
Plant Functional Genomics Research Group  
RIKEN Genomic Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-4359  
Fax: 81-298-36-9060  
Email: mseki@rtc.riken.go.jp  
An Arabidopsis full-length cDNA library was constructed essentially  
as reported previously (Seki et al., 1998). This clone is in a  
modified pBluescript vector as a SstI/XhoI insert. Please visit our  
web site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for  
further details.

FEATURES  
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/lab\_host="DH10B"  
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hr) treatments"  
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ORIGIN

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Matches 336; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
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QY 174 AAGACATATTAGGGAGCAGCTGAATCAAAGGAGGAAGAAGAAGAGAGCCCTTTTG 233  
Db |||||  
291 AAGACATATTAGGGAGCAGCTGAATCAAAGGAGGAAGAAGAAGAGAGCCCTTTTG 232  
QY 234 AGGCCATTCATGAATTTGGAATGAAGGATATCAAGAATCTAACACAAAGGCCGCTCT 293  
Db |||||  
231 AGGCCATTCATGAATTTGGAATGAAGGATATCAAGAATCTAACACAAAGGCCGCTCT 172  
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171 TCCTTCAATCTTTCCCTCTTTGAACTAAATAATTTTCATCCTTTCTCTCTCTGTCCT 112  
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Db |||||  
111 GGTCTTTTCTAGCTCAAAGTATCCTCATTTATGTCAAAGTGTGTAAATTCCTCAAGAC 52  
QY 414 TATATATGAGATGTTTGTTCATTTTCCAAATTTCAAACTTTGTGCCCC 463  
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Job time : 8562.19 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 23, 2003, 18:53:22 ; Search time 15516.7 Seconds  
(without alignments)  
11452.890 Million cell updates/sec

Title: US-10-084-553-1

Perfect score: 4344

Sequence: 1 gcagtggttcacttaaga.....actcataagtaagcacaaaa 4344

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2889711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:

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2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sta:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
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22: em\_ov:\*  
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25: em\_pl:\*  
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27: em\_sta:\*  
28: em\_un:\*  
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31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
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34: em\_htg\_pln:\*  
35: em\_htg\_ror:\*  
36: em\_htg\_nam:\*  
37: em\_htg\_vit:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	4344	100.0	4344	6	BD107660	BD107660 Phytochro
2	4344	100.0	5242	8	ATU79156	U79156 Arabidopsis
3	4310	99.2	68415	8	AC005310	AC005310 Arabidops
4	2092.2	48.2	2684	8	AY050961	AY050961 Arabidops
5	1527.6	35.2	2254	6	BD107661	BD107661 Phytochro
6	1525.2	35.1	2240	8	ATU28422	U28422 Arabidopsis
7	1349.2	31.1	1827	6	AX506805	AX506805 Sequence
8	1342	30.9	1612	8	BT001096	BT001096 Arabidops
9	1342	30.9	1612	8	BT001105	BT001105 Arabidops
10	1134	26.1	1134	6	AX509497	AX509497 Sequence
11	306.6	7.1	895	8	AY086711	AY086711 Arabidops
12	305.6	7.0	906	8	AY065156	AY065156 Arabidops
13	223.4	5.1	318	8	AY166504	AY166504 Arabidops
14	168.6	3.9	632	8	AY114583	AY114583 Arabidops
15	126	2.9	126	8	ATHS30832	ATHS30832 Arabidops
16	126	2.9	126	8	ATHS30917	ATHS30917 Arabidops
17	126	2.9	126	8	ATHS31369	ATHS31369 Arabidops
18	118.2	2.7	86436	8	AC007323	AC007323 Genomic s
19	101.6	2.3	95327	8	AC011354	AC011354 Genomic s
20	100	2.3	96232	8	ATAC010927	ATAC010927 Arabidops
21	99.2	2.3	75188	8	AB005238	AB005238 Arabidops
22	90.4	2.1	666	6	A68433	A68433 Sequence 6
23	88.4	2.0	151517	2	AP005750	AP005750 Oryza sat
24	88.4	2.0	167114	2	AP004685	AP004685 Oryza sat
25	85.8	2.0	2172	8	PVU420902	PVU420902 Phaseolus
26	85	2.0	124212	8	AC126787	AC126787 Medicago
27	84.2	1.9	131006	2	AC137985	AC137985 Medicago
28	83.2	1.9	2526	6	A68428	A68428 Sequence 1
29	83.2	1.9	2526	8	ATAJ6404	ATAJ6404 Arabidops
30	82.8	1.9	148626	8	AP004460	AP004460 Oryza sat
31	81.6	1.9	1938	6	AX506421	AX506421 Sequence
32	72.8	1.7	186315	8	OSJN00188	OSJN00188 Oryza sat
33	72.8	1.7	229796	2	AC137597	AC137597 Oryza sat
34	72.4	1.7	2160	6	AX660076	AX660076 Sequence
35	70.8	1.6	451	6	AX660581	AX660581 Sequence
36	66.4	1.5	349980	6	AX344550	AX344550 Sequence
37	66	1.5	120335	2	AP004255	AP004255 Oryza sat
38	66	1.5	204292	2	AP004071	AP004071 Oryza sat
39	65.4	1.5	8524	6	AX251342	AX251342 Sequence
40	65.4	1.5	8524	6	AX346743	AX346743 Sequence
41	64.4	1.5	331039	3	AC116988	AC116988 Dictyoste
42	64.2	1.5	1072	8	AY114070	AY114070 Arabidops
43	64.2	1.5	1429	8	AY063952	AY063952 Arabidops
44	63.8	1.5	182871	3	AC117176	AC117176 Dictyoste
45	63.4	1.5	134971	2	AC116367	AC116367 Oryza sat

# ALIGNMENTS

RESULT 1	BD107660	Phytochrome regulated transcription factor for control of higher	4344 bp	DNA	linear	PAT 18-SEP-2002
LOCUS	BD107660	plant development.				
DEFINITION	BD107660	plant development.				
ACCESSION	BD107660					
VERSION	BD107660.1	GI:23202478				
KEYWORDS	JP 2002501381-A/1.					
SOURCE	unidentified					
ORGANISM	unidentified					
REFERENCE	1 (bases 1 to 4344)					
AUTHORS	Tobin,R., Sun,L. and Wang,Z.Y.					
TITLE	Phytochrome regulated transcription factor for control of higher					
	plant development					



QY	1741	TCATCTTCATTGGCTTAATGCTTAAGACTTAATGAAAGCCAGGCAAGTTTCTGCTTCTT	1800
DB	1741	TCATCTTCATTGGCTTAATGCTTAAGACTTAATGAAAGCCAGGCAAGTTTCTGCTTCTT	1800
QY	1801	TTGCTTCTTAGTCAGGAGATAGATAGATTACGTTTTTTAGAGTTTTAGTAATGACCAATAAG	1860
DB	1801	TTGCTTCTTAGTCAGGAGATAGATAGATTACGTTTTTTAGAGTTTTAGTAATGACCAATAAG	1860
QY	1861	TCTTAAAAATAGTTGGAGAAATGACGAGATGTAATCGTTTTCTTTTGTGTTATGCTTATATC	1920
DB	1861	TCTTAAAAATAGTTGGAGAAATGACGAGATGTAATCGTTTTCTTTTGTGTTATGCTTATATC	1920
QY	1921	TTGTTAATCCACAAACATGTACATAGATTCTTCAGAGAAATGTTAGTTTCTTTAGATTCT	1980
DB	1921	TTGTTAATCCACAAACATGTACATAGATTCTTCAGAGAAATGTTAGTTTCTTTAGATTCT	1980
QY	1981	TCAGATAAACTTGTGCTTCTTACCAGATTCTGAGGTAGTGCCAAAAAGTGGGCTGAGTGCT	2040
DB	1981	TCAGATAAACTTGTGCTTCTTACCAGATTCTGAGGTAGTGCCAAAAAGTGGGCTGAGTGCT	2040
QY	2041	AGAAATTTTGTAAATGTTCTTGTGATAAGCCATAGAGGTAAACCATTTTTGTATTTCCAG	2100
DB	2041	AGAAATTTTGTAAATGTTCTTGTGATAAGCCATAGAGGTAAACCATTTTTGTATTTCCAG	2100
QY	2101	TTCTGTCAATTAACCTTGTAGGTGTCATTAGATTCTTTGTTGTTTACGTTTGTAGAG	2160
DB	2101	TTCTGTCAATTTAACTTGTAGGTGTCATTAGATTCTTTGTTGTTTACGTTTGTAGAG	2160
QY	2161	GGTAAACAAACTACTCTCATCTCTCAGGTAGAGAAAGGCTGAAGCTTAAAGGTGTAG	2220
DB	2161	GGTAAACAAACTACTCTCATCTCTCAGGTAGAGAAAGGCTGAAGCTTAAAGGTGTAG	2220
QY	2221	CTATGGGTCAAGCGCTAGACATAGCTATTCTCTCCACGCGCTAAGCGTAAACCAACA	2280
DB	2221	CTATGGGTCAAGCGCTAGACATAGCTATTCTCTCCACGCGCTAAGCGTAAACCAACA	2280
QY	2281	ATCTCTTATCCTGAAAGCGGGAAGTGGACGATCCTTATGTCAAAAACGGGTGTAATG	2340
DB	2281	ATCTCTTATCCTGAAAGACGGGAAGTGGACGATCCTTATGTCAAAAACGGGTGTAATG	2340
QY	2341	ATGGAAAGAGTCCCTTGGATCAGAAAAAGTGTGCGATCCTGAGGTGATTTTCATGGTCA	2400
DB	2341	ATGGAAAGAGTCCCTTGGATCAGAAAAAGTGTGCGATCCTGAGGTGATTTTCATGGTCA	2400
QY	2401	TATGGCATCTTTTTCAGTGTGTACATTGCTCTCATGTTATTAATACAGATTGTGTGC	2460
DB	2401	TATGGCATCTTTTTCAGTGTGTACATTGCTCTCATGTTATTAATACAGATTGTGTGC	2460
QY	2461	TTTCGTTTATAGATGGCCCAATGAAGATCGACAACATCAAGCCTGAAGACAACTCTGC	2520
DB	2461	TTTCGTTTATAGATGGCCCAATGAAGATCGACAACATCAAGCCTGAAGACAACTCTGC	2520
QY	2521	AGGAAGCAACTGTTTCAGATTGTTTTCATCTCATCAGTATCTCTGCTGCACTCCTCCATGA	2580
DB	2521	AGGAAGCAACTGTTTCAGATTGTTTTCATCTCATCAGTATCTCTGCTGCACTCCTCCATGA	2580
QY	2581	ATAAAAGTTGTATAGAGACATCAAAACGCAAGCACTTTCGCGAGTTCTTCCGCTTACGGG	2640
DB	2581	ATAAAAGTTGTATAGAGACATCAAAACGCAAGCACTTTCGCGAGTTCTTCCGCTTACGGG	2640
QY	2641	AAGAGGTAAAAACAATCTTTTCATCTGCTATTTGAGGTTTTTAAGACGATTAGTACTTTTCA	2700
DB	2641	AAGAGGTAAAAACAATCTTTTCATCTGCTATTTGAGGTTTTTAAGACGATTAGTACTTTTCA	2700
QY	2701	TGAAACTAAAAACGTTGGGGAATTAACAGGGAAGTCAGAAATTAACAGGGTAAGAAAGGATC	2760
DB	2701	TGAAACTAAAAACGTTGGGGAATTAACAGGGAAGTCAGAAATTAACAGGGTAAGAAAGGATC	2760
QY	2761	AAACTCAGATTGAAATGCAAAATCTCTCGAAACCGGTAAATAGCAAGGACCTCAGACTTA	2820
DB	2761	AAACTCAGATTGAAATGCAAAATCTCTCGAAACCGGTAAATAGCAAGGACCTCAGACTTA	2820
QY	2821	TCCGATGCATATCCCTGTGCTAGTGCCATTGGGGAGCTCAATAACAAGTTCTCTATCACA	2880

DB	2821	TCCGATGCATATCCCTGTGCTAGTGCCATTGGGGAGCTCAATAACAAGTTCTCTATCACA	2880
QY	2881	TCCTCTCTCAGAGCCAGATAGTATCCACACAGTTGCAGGAGATTATCAGTCGTTTCC	2940
DB	2881	TCCTCTCTCAGAGCCAGATAGTATCCACACAGTTGCAGGAGATTATCAGTCGTTTCC	2940
QY	2941	TAAATCATATAATGTCAACCCCTTTTACAAAACACCGGCTCTTTTATATGTCGCCCAACTTCGC	3000
DB	2941	TAAATCATATAATGTCAACCCCTTTTACAAAACACCGGCTCTTTTATATGTCGCCCAACTTCGC	3000
QY	3001	CTCATCATTTTGGCTCCCGATTCTAGTGGTGCTCACCTGTTCCAGGGAACTCACCTCC	3060
DB	3001	CTCATCATTTTGGCTCCCGATTCTAGTGGTGCTCACCTGTTCCAGGGAACTCACCTCC	3060
QY	3061	GAATCTGGCTGCCATGGCCGACCACTGTTGAGCTGCTAGTGTCTTGGTGGGCTGCCAA	3120
DB	3061	GAATCTGGCTGCCATGGCCGACCACTGTTGAGCTGCTAGTGTCTTGGTGGGCTGCCAA	3120
QY	3121	TGGATTATTAACCTTTATGTGCTCTCTTATAGTTCAGGTGGTTTCACTAGTCATCTCCATC	3180
DB	3121	TGGATTATTAACCTTTATGTGCTCTCTTATAGTTCAGGTGGTTTCACTAGTCATCTCCATC	3180
QY	3181	TACTTTTGGACCATCATGTGATAGTAGTACACAAAAGCAAGCACTTTTACAAATGTTTC	3240
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QY	3241	TGTGACAGCCGAGAGCAAGAACACCTCCGAGGATCAAAAGGCTCGATCTTCACTGGAATC	3300
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QY	3361	GAGTGTGCAAAAGGTTTCAAGTGGAGCAGAGACAGAAAACAAGTTGACCGGCTCTCGT	3420
DB	3361	GAGTGTGCAAAAGGTTTCAAGTGGAGCAGAGACAGAAAACAAGTTGACCGGCTCTCGT	3420
QY	3421	TGGCTCAAAACACTCCGCTCGAGTAGTATGATGTTGAGGGGATGCAATCAAGAGGCAAGA	3480
DB	3421	TGGCTCAAAACACTCCGCTCGAGTAGTATGATGTTGAGGGGATGCAATCAAGAGGCAAGA	3480
QY	3481	GGATGSCACCAATGTTGAGGTGAAAGAAACGAATGAAGACACTAATAAAACCTCAAACTTC	3540
DB	3481	GGATGSCACCAATGTTGAGGTGAAAGAAACGAATGAAGACACTAATAAAACCTCAAACTTC	3540
QY	3541	AGAGTCCAATGACGCCGCGAGTAGAATCAGCTTCCAAATATAACCGATCCATGGGAAGTCTGT	3600
DB	3541	AGAGTCCAATGACGCCGCGAGTAGAATCAGCTTCCAAATATAACCGATCCATGGGAAGTCTGT	3600
QY	3601	GTCTGACGAGGTACTTTTACCTTGGACTAAAGATCAACTTCTTTTATTTTCAATCATTTTCTC	3660
DB	3601	GTCTGACGAGGTACTTTTACCTTGGACTAAAGATCAACTTCTTTTATTTTCAATCATTTTCTC	3660
QY	3661	ATATAAATATGTPACATTCGGGTGCAATTCGCTTCCAAAGCTCTTCTTCCAGAGAGGTAT	3720
DB	3661	ATATAAATATGTPACATTCGGGTGCAATTCGCTTCCAAAGCTCTTCTTCCAGAGAGGTAT	3720
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DB	3721	TGCCGCAAAAGTTTACATATCGAGAAGAACACAGAGAGGAAGAACAAACAACAAGAAC	3780
QY	3781	AAAGATATCCAATGGCAGTTGATCTTAACTTCCAGCTCAGTTTAAACCCAGTTTGTATGATC	3840
DB	3781	AAAGATATCCAATGGCAGTTGATCTTAACTTCCAGCTCAGTTTAAACCCAGTTTGTATGATC	3840
QY	3841	AAAGAGAGAGAGAAACAAGATTCTTGGAAATCGGATTTAGATGCTTCAAAAGCTAATGA	3900
DB	3841	AAAGAGAGAGAGAGAAACAAGATTCTTGGAAATCGGATTTAGATGCTTCAAAAGCTAATGA	3900
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DEFINITION complete cds.  
ACCESSION U79156  
VERSION U79156.1 GI:4090568  
KEYWORDS Arabidopsis thaliana (thale cress)  
SOURCE Arabidopsis thaliana  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
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REFERENCE 1 (bases 1 to 5242)  
Wang,Z.-Y., Kenigsbuch,D., Sun,L., Harel,E., Ong,M.S. and Tobin,E.M.  
A Myb-related transcription factor is involved in the phytochrome  
regulation of an Arabidopsis Lhcb gene  
Plant Cell 9 (4), 491-507 (1997)  
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2 (bases 1 to 5242)  
Wang,Z.-Y., Kenigsbuch,D., Sun,L., Harel,E., Ong,M.S. and  
Tobin,E.M.  
Direct Submission  
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QY 1621 ACTGATTTTCTTTTTCATTTTGGACAGAACATGTAGCAACAAAACTGCTGTCCAGATA 1680  
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## RESULT 3

AC005310

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

AUTHORS

TITLE

JOURNAL

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1 (bases 1 to 68415)  
Rounsley, S.D., Lin, X., Kaul, S., Shea, T.P., Fujii, C.Y., Mason, T.M.,  
Shen, M., Ronning, C.M., Fraser, C.M., Somerville, C.R. and Venter, J.C.  
2 (bases 1 to 68415)  
Unpublished  
Lin, X.

Direct Submission  
Submitted (09-MAR-2000) The Institute for Genomic Research, 9712  
Medical Center Dr., Rockville, MD 20850, USA

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REFERENCE 3 (bases 1 to 68415)
AUTHORS Town,C.D. and Kaul,S.
TITLE Direct Submission
JOURNAL Submitted (27-FEB-2002) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA, cdtown@igr.org
COMMENT On Apr 18, 2002 this sequence version replaced gi:698455.
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Best Local Similarity 88.1%; Pred No 5 7e-306.

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LOCUS		Arabidopsis thaliana clone C105127 (D) putative MYB-related	
DEFINITION		transcription factor CCAL (At2g46830) mRNA, complete cds.	
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AUTHORS		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	
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		1 (bases 1 to 1612)	
		Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M.,	
		Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C.,	
		Yu, G., Yuan, S., Chen, H., Cheuk, R., Jones, T., Kim, C.J., Nguyen, M.,	
		Palm, C.J., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Davis, R.W.,	
		Ecker, J.R. and Theologis, A.	
TITLE		Arabidopsis Open Reading Frame (ORF) Clones	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 1612)	
AUTHORS		Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M.,	
		Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C.,	
		Yu, G., Yuan, S., Chen, H., Cheuk, R., Jones, T., Kim, C.J., Nguyen, M.,	
		Palm, C.J., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Davis, R.W.,	
		Ecker, J.R. and Theologis, A.	
TITLE		Direct Submission	
JOURNAL		Submitted (30-OCT-2002) Plant Gene Expression Center, 800 Buchanan	
COMMENT		Street, Albany, CA 94710, USA	
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Qy	2763	ACTCAGATTTGAATGCAAAAATCTCTGGAACCGTAAATGACAAAGGACCTCAGACTTATC	2822	
Db	371	ACTCAGATTTGAATGCAAAAATCTCTGGAACCGTAAATGACAAAGGACCTCAGACTTATC	430	
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Qy	2883	CTCCTTCAGAGCCAGATAGTATCCCCACACAGTTGAGAGATTTATCAGTCGTTTCTCTA	2942	
Db	491	CTCCTTCAGAGCCAGATAGTATCCCCACACAGTTGAGAGATTTATCAGTCGTTTCTCTA	550	
Qy	2943	ATCATATAATGTCAACCCCTTTTAAACACCGGCTCTTTATCTATCTCCGCAACTTTCGCT	3002	
Db	551	ATCATATAATGTCAACCCCTTTTAAACACCGGCTCTTTATCTATCTCCGCAACTTTCGCT	610	
Qy	3003	CATCATTTTGGCCTCCCGATTCTTAGTGGTGGCTCACTGTTCAGGGAACCTCACCTCGA	3062	
Db	611	CATCATTTTGGCCTCCCGATTCTTAGTGGTGGCTCACTGTTCAGGGAACCTCACCTCGA	670	

QY 3063 ATCTGGCTGCATGGCGGCGGCACTGTTGCAGCTGCTAGTGTCTTGGTGGCTGCCAATG 3122  
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Db 1381 GAGGAGAGAGAAACACAGAGATTTCTTGGAAATCGGATAGATGCTTCAAAGCTTAATGAGT 1440  
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QY 3903 AGAGGAGAGAAACAGGTTTAAACCATACAAAGATGTTCCATGGAAGCCAAAGAAAGTAGA 3962  
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QY 3963 ATCTCTCAACAAACCTATCATTTTCATGTTGGAACAGAAAGATCCCAAGCGATGCGGTTG 4022  
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Db 1501 ATCTCTCAACAAACCTATCATTTTCATGTTGGAACAGAAAGATCCCAAGCGATGCGGTTG 1560  
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QY 4023 GAAACTCAAGCTTCCACATGAGACTCTATTTTTCATCTGATCTGTTGTTGTA 4074  
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Db 1561 GAAACTCAAGCTTCCACATGAGACTCTATTTTTCATCTGATCTGTTGTTGTA 1612  
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RESULT 9  
BT001105  
LOCUS Arabidopsis thaliana clone Cl05127 (D) putative MYB-related  
DEFINITION

transcription factor CCA1 (At2g46830) mRNA, complete cds.  
BT001105  
BT001105.1 GI:24762204  
FLI CDNA.  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 1612)  
Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M.,  
Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C.,  
Yu, G., Yuan, S., Chen, H., Cheuk, R., Jones, T., Kim, C.J., Nguyen, M.,  
Palm, C.J., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Davis, R.W.,  
Ecker, J.R. and Theologis, A.  
Arabidopsis Open Reading Frame (ORF) Clones  
Unpublished  
2 (bases 1 to 1612)  
Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M.,  
Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C.,  
Yu, G., Yuan, S., Chen, H., Cheuk, R., Jones, T., Kim, C.J., Nguyen, M.,  
Palm, C.J., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Davis, R.W.,  
Ecker, J.R. and Theologis, A.  
Direct Submission  
Submitted (07-NOV-2002) Plant Gene Expression Center, 800 Buchanan  
Street, Albany, CA 94710, USA  
Annotation based on July 2002 version of the Arabidopsis genome  
submitted to Genbank.

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LSHPSEPDSPHPTVAGDYQSPFNHIMSTLLQTPALYATATFASFPDPSGSPVP  
GNSPNLAAMAAATVAASAAWAAAGLLPLCAPLSSGFTSPHPSTFGPSCDVEYTKA  
STLQHSVQSEHESEASKARSLDSEVENKSKPVCHQEPSATPESDAKSGDAGD  
RKQVRSSCGSNTPSSDDVEADASEEDGTEKNETNEDNKTPOTSSNARRSI  
SSNITDPMKVSDEGRIFALFREVLPSTFYREEHREEEQOQEQRYPMALDINF  
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505 a 366 c 360 g 381 t

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Matches 1612; Conservative 0; Mismatches 0; Indels 240; Gaps 3;  
QY 2223 ATGGGTCAAGCGCTAGACATAGCTATTCTCTCCACGCGCTTAAGCGTAACCAACAAT 2282  
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Db 1 ATGGGTCAAGCGCTAGACATAGCTATTCTCTCCACGCGCTTAAGCGTAACCAACAAT 60  
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QY 2283 CCTTATCTCGAAGACGGAAGTGGACGATCTTATGTCAAAAACGGGTGTAATGAT 2342  
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Db 61 CCTTATCTCGAAGACGGAAGTGGACGATCTTATGTCAAAAACGGGTGTAATGAT 120  
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[illegible]

QY	1278	GATTAGTGGAAATTTTGTAAAGAGAGATCTGAAGTTGTGTAGAGGAGCTTAGTG	1331
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RESULT 11			
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LOCUS	AY086711	895 bp	linear
DEFINITION	Arabidopsis thaliana clone 26967 mRNA, complete sequence.		
ACCESSION	AY086711		
VERSION	AY086711.1	GI:21405421	
KEYWORDS	FLI CDNA.		
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
AUTHORS	1 (bases 1 to 895) Haas,B.J., Volkovskiy,N., Town,C.D., Troukhan,M., Alexandrov,N., Feldmann,K., Flavell,R.B., White,O. and Salzberg,S.L.		
TITLE	Full-length messenger RNA sequences greatly improve genome annotation		
JOURNAL	Genome Biol. 3 (6), RESEARCH0029 (2002)		
MEDLINE	22088475		
PUBMED	12093376		
REFERENCE	2 (bases 1 to 895)		
AUTHORS	Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.		
TITLE	Full-Length cDNA from Arabidopsis thaliana		
JOURNAL	Unpublished		
REFERENCE	3 (bases 1 to 895)		
AUTHORS	Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA		
COMMENT	This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or Laer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. GenSet carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.		
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BASE COUNT	224 a	208 c	175 g
ORIGIN	288 t		
Query Match	7.1%	Score 306.6;	DB 8; Length 895;
Best Local Similarity	95.7%	Pred. No. 5.2e-53;	



	Matches	315;	Conservative	0;	Mismatches	14;	Indels	0;	Gaps	0;	
Qy	114	AGGAAA	TTGTTT	GTAT	CTCT	TTTCAGGGAGG	CTTT	GTGTTGAGAAAGGT	CAAGAGCACATAC	173	
Db	567	AAGAAC	CTGGT	CTTT	CAAA	ACCAGACAGAGG	GGCTTT	GTGTTTGAGAAGGT	CAAGAGCACATAC	626	
Qy	174	AAAGAC	ATATT	AGGAGCAG	CTG	GAATCAA	AGGAGGAAGA	GAAGAAGAGAGC	CTTTTTG	233	
Db	627	AAAGAC	ATATT	AGGAGCAG	CTG	GAATCAA	AGGAGGAAGA	GAAGAAGAGAGC	CTTTTTG	686	
Qy	234	AGGCCA	TTCA	TGAAT	TGGAAT	GAAGGATATCAA	AAAGAACTCT	AACACAAAGGCC	ACGTCCT	293	
Db	687	AGGCCA	TTCA	TGAAT	TGGAAT	GAAGGATATCAA	AAAGAACTCT	AACACAAAGGCC	ACGTCCT	746	
Qy	294	TCCTT	CAATCT	TTT	CCCTTT	GTAACTAA	ATAATTT	TCATCCTTT	CTCTCTCTGTCCT	353	
Db	747	TCCTT	CAATCT	TTT	CCCTTT	GTAACTAA	ATAATTT	TCATCCTTT	CTCTCTCTGTCCT	806	
Qy	354	GGTCT	TTTTT	TAGCT	CAAA	GTATCAT	CTCATTT	TATGTCAAAGT	TGTTGTAATTCCT	CAAGAC	413
Db	807	GGTCT	TTTTT	TAGCT	CAAA	GTATCAT	CTCATTT	TATGTCAAAGT	TGTTGTAATTCCT	CAAGAC	866
Qy	414	TATAT	ATGAG	ATGTTTT	TGTTT	GCATTT	TCC	442			
Db	867	TATAT	ATGAG	ATGTTTT	TGTTT	GCATTT	TCC	895			

RESULT 12	AY065156	1000 bp	linear	PLN 10-DEC-2001
LOCUS	AY065156			
DEFINITION	Arabidopsis thaliana unknown protein (At2g46820; F19D11.10) mRNA, complete cds.			
ACCESSION	AY065156			
VERSION	AY065156.1	GI:17473793		
KEYWORDS	FLI CDNA.			
SOURCE	Arabidopsis thaliana (thale cress)			
ORGANISM	Arabidopsis thaliana			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots; rosids; eustoids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 906)			
AUTHORS	Nguyen, M., Karlin-Neumann, G., Southwick, A., Lam, B., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H., Cheuk, R., Chung, M.K., Hayashizaki, Y., Ishida, J., Kamiya, A., Kawai, J., Kim, C., Lin, J., Liu, S.X., Narusaka, M., Pham, P.K., Sakano, H., Sakurai, T., Satou, M., Seki, M., Shimizu, Y., Yamada, K., Shinozaki, K., Ecker, J., Theologis, A. and Davis, R.W.			
TITLE	Direct Submission			
JOURNAL	Submitted (03-DEC-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA			

COMMENT e-mail for correspondence: arab@sequence.stanford.edu  
USA

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA') : Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Nguyen, M., Southwick, A., Kari-Niemann, G., Lam, B., Miranda, M., Palm, C. J., Bowser, L., Jones, T., Bah, J., Chen, H., Cheuk, R., Chung, M. K., Kim, C., Lin, J., Liu, S. X., Pham, P. K., Sakano, H., Shinn, P., Yamada, K., Ecker, J., Theologis, A. and Davis, R. W.

Nguyen, M., (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W. (SSP/Stanford) contributed equally to this work as PIs.

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source
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Location/Qualifiers
/mol_type="mRNA"
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/db_xref="taxon:3702"
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gene

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Best Local Similarity 95.7%; Pred. No. 8.4e-53;  
Matches 314; Conservative 0; Mismatches 14; Indels 0

Qy	114	AGGAAATTGTTGTTATCTGTTTCAGGAGGCTTTGTTTGAGAAGGTCAAGAGCACATAC	173
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Qy	174	AAAGACATATTAGGAGCAGCTGAATCAAGGAGGAGAAAGAAAGAGACGCTTTTGTG	233
Db	639	AAAGACAATATTAGGAGCAGCTGAATCAAGGAGGAGAAAGAAAGAGACGCTTTTGTG	698
Qy	234	AGGCCATTGATGGAATCGGAATGAGGATATCAAAAGAACTCAACACAAGGCCAGCTCCT	293
Db	699	AGGCCATTGATGGAATCGGAATGGAAGSATATCAAAAGAACTCAACACAAGGCCAGCTCCT	758
Qy	294	TCCTTCAATCTTTCCTTCTTGTAATAAATTTTCATCCTTCTCTCTCTCTCTCTCTCT	353
Db	759	TCCTTCAATCTTTCCTTCTTGTAATAAATTTTCATCCTTCTCTCTCTCTCTCTCTCT	818
Qy	354	GGTCTTTTTTAGCTCAAAGTATCATCCATTTATGTCAAAGTGTGTAAATTCCTCAAGAC	413
Db	819	GGTCTTTTTTAGCTCAAAGTATCATCCATTTATGTCAAAGTGTGTAAATTCCTCAAGAC	878
Qy	414	TATATATGAGATGTTTTGTTTCATTTTC	441
Db	879	TATATATGAGATGTTTTGTTTCATTTTC	906

RESULT 13  
AY166504

AY166504	318 bp	linear	PLN 21-DEC-2002
LOCUS		mRNA	
DEFINITION	<i>Brassica rapa</i> subsp. <i>pekinensis</i> Myb-related transcription factor		
	CCAL mRNA, partial cds.		

ACCESSION AY166504  
VERSION AY166504.1 GI:27357049

KEYWORDS	SOURCE	ORGANISM
	Brassica rapa subsp.	pekinensis
	Brassica rapa subsp.	pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE  
AUTHORS  
1 (bases 1 to 318)  
Jang, H. and Hur, Y.

**TITLE** Study on the expression pattern of genes associated with flowering  
in chinese cabbage plants

JOURNAL  
REFERENCE  
Unpublished  
2 (bases 1 to 318)  
in chinese cabbage

REFERENCE	AUTHORS	TITLE
1	...	...
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**JOURNAL** Direct Submission  
**FEATURES** Submitted (16-OCT-2002) Biology, Chungnam National University, Kungdong, Yuseong-ku, Deajeon 305-764, Korea  
Location/Qualifiers

[illegible]

RESULT 14	
AY114583	
LOCUS	632 bp mRNA linear PLN 10-JUN-2002
DEFINITION	Arabisopsis thaliana unknown protein (Atg46820) mRNA, complete cds.
ACCESSION	AY114583
VERSION	AY114583.1 GI:21396996
KEYWORDS	FLI CDNA.
SOURCE	Arabisopsis thaliana (thale cress)
ORGANISM	Arabisopsis thaliana
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE	1 (bases 1 to 632)
AUTHORS	Tripp, M., Southwick, A., Karlin-Neumann, G., Nguyen, M., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H., Cheuk, R., Chung, M.K., Hayashizaki, Y., Ishida, J., Kamiya, A., Kawai, J., Kim, C., Lin, J., Liu, S.X., Narusaka, M., Pham, P.K., Sakano, H., Sakurai, T., Satou, M., Seki, M., Shim, P., Yamada, K., Shinozaki, K., Ecker, T.J., Theologis, A. and Davis, R.W.
TITLE	Direct Submission
JOURNAL	Submitted (22-MAY-2002) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
COMMENT	e-mail for correspondence: arab@sequence.stanford.edu

collection and clustering of RAFL cDNAs (RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, POEC (SSP) Consortium members constructed and sequenced the PUNI (ORF) clones using the RAFL cDNAs: Tripp,M., Nguyen,M., Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P., Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.

Tripp,M. (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIs.

FEATURES  
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 Matches 177; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
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 Qy 174 AAGACATATTAGGAGGACGCTGAATCAAGGAGGAAGAGAGAGAGAGAGGCTTTTGG 233  
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 ACCESSION AJ530832  
 VERSION AJ530832.1 GI:26799092  
 KEYWORDS left border; T-DNA flanking sequence.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2003, 18:46:12 ; Search time 1060.65 Seconds  
(without alignments)  
11055.799 Million cell updates/sec

Title: US-10-084-553-1

Perfect score: 4344

Sequence: 1 gcagtggttcacttacaaga.....actcataagtaagcacaaaa 4344

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4344	100.0	4344	19 AAV65381	Arabidopsis thalia
2	1527.6	35.2	2254	19 AAV65382	Arabidopsis thalia
3	1525.2	35.1	2240	22 AAD06664	A. thaliana trans
4	1525.2	35.1	2240	22 AAD05746	Arabidopsis thalia
5	1525.2	35.1	2240	22 AAD05773	Arabidopsis thalia
6	1349.2	31.1	1827	24 AB213695	Arabidopsis thalia
7	1134	26.1	1134	24 AB216387	Arabidopsis thalia
8	312.6	7.2	865	24 AEN98810	Arabidopsis thalia

9	306.6	7.1	846	21 AAC39815	Arabidopsis thalia
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11	304.6	7.0	844	21 AAC49446	Arabidopsis thalia
12	304.6	7.0	893	21 AAC47534	Arabidopsis thalia
13	121.2	2.8	507	21 AAC52051	Arabidopsis thalia
14	116.6	2.7	478	21 AAC41232	Arabidopsis thalia
15	94.4	2.2	2730	21 AAC47080	Arabidopsis thalia
16	90.4	2.1	666	19 AAV09298	Inverse PCR fragme
17	83.2	1.9	2526	19 AAV09298	Nucleotide sequenc
18	83.2	1.9	2526	22 AAD06648	A. thaliana trans
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22	81.6	1.9	1938	24 AB213111	Arabidopsis thalia
23	66.8	1.5	592	25 ABX56693	Arabidopsis thalia
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25	65.4	1.5	8524	24 ABLJ3841	Human immune syste
26	62.8	1.4	1148	21 AAC45095	Arabidopsis thalia
27	62.8	1.4	1330	21 AAC38730	Arabidopsis thalia
28	62.8	1.4	26997	22 AAS46747	Tumour suppressor
29	62.4	1.4	15373	24 ABL32466	Human immune syste
30	61.6	1.4	525	24 AB214536	Arabidopsis thalia
31	60	1.4	320	21 AAC56865	Eucalyptus grandis
32	59.8	1.4	17594	24 ABLJ4026	Human immune syste
33	59.6	1.4	12138	24 ABLJ3342	Human immune syste
34	59.6	1.4	12138	24 ABK28335	DNA transcription
35	59.4	1.4	6115	24 ABLJ3801	Human immune syste
36	59	1.4	5586	24 ABK40004	Human chemically p
37	58.8	1.4	40324	24 ABO67150	Human angiogenesis
38	58.4	1.3	411	25 ABX49356	Bovine EST associa
39	57.6	1.3	8079	24 ABL92313	Chemically treated
40	57.4	1.3	6095	22 AAS46310	Tumour suppressor
41	57.4	1.3	6095	24 ABL70150	Chemically treated
42	57.4	1.3	6095	24 ABLJ2361	Human immune syste
43	57.4	1.3	6095	24 ABLJ4475	Human metastasis a
44	57.4	1.3	61020	22 AAS46788	Tumour suppressor
45	57	1.3	7455	24 ABLJ3759	Human immune syste

#### ALIGNMENTS

RESULT 1

AAV65381

ID AAV65381 standard; DNA; 4344 BP.

XX

AC AAV65381;

XX

DT 15-FEB-1999 (first entry)

XX

DE Arabidopsis phytochrome regulated transcription factor CCAL DNA.

XX

KW Phytochrome regulated transcription factor; CCAL;

KW chlorophyll binding protein; lhcb1\*3; circadian rhythm; flowering;

KW transgenic plant; ss.

XX

OS Arabidopsis thaliana ecotype Columbia.

XX

PH Key Location/Qualifiers

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FT /note= "contains introns"

FT exon 1..1999

FT /tag= b

FT /number= 1

FT intron 1200..1283

FT /tag= c

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FT intron 1371..1448

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 PF 17-APR-1998; 98WO-US07693.  
 PR 18-APR-1997; 97US-0843572.  
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 PA (REGC ) UNIV CALIFORNIA.  
 DR WPI; 1998-583656/49.  
 DR P-PSDB; AAW79280.  
 XX XX  
 PT Alteration of plant circadian rhythms - by transformation with a  
 PT transcription factor for the promoter of the Arabidopsis chlorophyll  
 PS binding protein  
 PS Claim 1; Page 36-40; 47pp; English.  
 CC This genomic DNA sequence codes for a phytochrome-regulated  
 CC transcription factor, designated CCA1 (see AAW79280), that binds to  
 CC the promoter region of the chlorophyll binding protein gene  
 CC (Lhcb1.3) of Arabidopsis thaliana. The genomic clone was  
 CC by screening an Arabidopsis ecotype Columbia genomic library using  
 CC CCA1 cDNA (see AAW65382) as probe. A claimed method for altering  
 CC plant response to daylength comprises transforming a plant with  
 CC either the CCA1 genomic DNA or cDNA, a hybridizing sequence or a  
 CC nucleic acid encoding a protein containing amino acids 24-75 of the  
 CC 608-amino acid CCA1 protein. Manipulation of plant circadian  
 CC rhythms (e.g. by overexpression of CCA1) can be used to delay  
 CC flowering, and thus increase yield from both forage crops, where  
 CC biomass will be produced for longer, and from seed crops such as  
 CC rape, where a longer time in vegetative state will lead to larger  
 CC plants and thus a higher seed set (claimed).  
 XX SQ Sequence 4344 BP; 1303 A; 808 C; 883 G; 1350 T; 0 other;  
 Query Match 100.0%; Score 4344; DB 19; Length 4344;

Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 DB |||||  
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QY 3421 TGCGTCAACACCTCCGTCGAGTAGTGATGTTGAGGCGGATGCATCAGAAAGGCAAGA 3480  
DB 3421 TGCGTCAACACCTCCGTCGAGTAGTGATGTTGAGGCGGATGCATCAGAAAGGCAAGA 3480  
QY 3481 GGATGGCACCACATGGTGAGGTGAAAGAAACGAATGAAGACACTAATAAACCCTCAAACTTC 3540  
DB 3481 GGATGGCACCACATGGTGAGGTGAAAGAAACGAATGAAGACACTAATAAACCCTCAAACTTC 3540  
QY 3541 AGAGTCCAATGCAAGCGCGAGTAGAATCAGCTCCAATATAACCGATCCATGGAAGTCTGT 3600  
DB 3541 AGAGTCCAATGCAAGCGCGAGTAGAATCAGCTCCAATATAACCGATCCATGGAAGTCTGT 3600  
QY 3601 GTCTGACGAGTACTTCTTGGACTAAGATCAATCACTTCTTTTCAAAATCATTTTCTC 3660  
DB 3601 GTCTGACGAGTACTTCTTGGACTAAGATCAATCACTTCTTTTCAAAATCATTTTCTC 3660  
QY 3661 ATATAAATATGTTACATTTGGGTCGAATTCGCTTCCAAAGTCTCTTCTCCAGAGAGGTAT 3720  
DB 3661 ATATAAATATGTTACATTTGGGTCGAATTCGCTTCCAAAGTCTCTTCTCCAGAGAGGTAT 3720  
QY 3721 TGCGCGAAAGTTTACATATCGAAGAAACACAGAGAGGAAGAACAAACAAACAAGAAC 3780  
DB 3721 TGCGCGAAAGTTTACATATCGAAGAAACACAGAGAGGAAGAACAAACAAACAAGAAC 3780  
QY 3781 AAGATATCAATGGGCACTTGATCTTAACTTTCACAGCTCAGTTAAACACAGTTGATGATC 3840  
DB 3781 AAGATATCAATGGGCACTTGATCTTAACTTTCACAGCTCAGTTAAACACAGTTGATGATC 3840  
QY 3841 AAGAGGAGAGAGAAACACAGGATTTCTTGGAAATCGGATAGATGCTTCAAGCTTAATGA 3900  
DB 3841 AAGAGGAGAGAGAAACACAGGATTTCTTGGAAATCGGATAGATGCTTCAAGCTTAATGA 3900  
QY 3901 GTAGAGAGAGAGAGAGGTTTAAACCATACAAAGATGTTCCATGGAAGCGCAAGAAAGTA 3960  
DB 3901 GTAGAGAGAGAGAGAGGTTTAAACCATACAAAGATGTTCCATGGAAGCGCAAGAAAGTA 3960  
QY 3961 GAATCTCTCAACAACATCTTATCATCTGGAACAGAAAGATCCCAACCGGATCGGT 4020  
DB 3961 GAATCTCTCAACAACATCTTATCATCTGGAACAGAAAGATCCCAACCGGATCGGT 4020  
QY 4021 TGGAAACTCAAGCTTCCACATGAGACTCTATTTTTCATCTGATCTGTTGTTGTTACTCTGT 4080  
DB 4021 TGGAAACTCAAGCTTCCACATGAGACTCTATTTTTCATCTGATCTGTTGTTGTTACTCTGT 4080  
QY 4081 TTTTAAGTTTTCAGACCACTGCTACATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 4140  
DB 4081 TTTTAAGTTTTCAGACCACTGCTACATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 4140  
QY 4141 TCCTGTGCAATGCTTCTGTAACATTTGACTCTGTATTTTCAACAAATCAATAACTG 4200  
DB 4141 TCCTGTGCAATGCTTCTGTAACATTTGACTCTGTATTTTCAACAAATCAATAACTG 4200  
QY 4201 TTTTAATCTTTTTCACCTCGAAGAAATTTCACTCAAGGGGCTTCTGTTCTTGATA 4260  
DB 4201 TTTTAATCTTTTTCACCTCGAAGAAATTTCACTCAAGGGGCTTCTGTTCTTGATA 4260  
QY 4261 TATGCAAAACGACAGAGTTTCAAAACGTAATCTTTAGCCCATTCATCAACCTTAAAGTTGCT 4320  
DB 4261 TATGCAAAACGACAGAGTTTCAAAACGTAATCTTTAGCCCATTCATCAACCTTAAAGTTGCT 4320  
QY 4321 CATAACTCATAAGTAAGCACAAA 4344

DB 4321 CATAACTCATAAGTAAGCACAAA 4344  
RESULT 2  
AAV65382  
ID AAV65382 standard; cDNA to mRNA; 2254 BP.  
XX AAV65382;  
AC AC  
XX 15-FEB-1999 (first entry)  
DT  
XX  
DE Arabidopsis phytochrome regulated transcription factor CCA1 cDNA.  
XX  
KW Phytochrome regulated transcription factor; CCA1;  
KW chlorophyll binding protein; Lhcb1\*3; circadian rhythm; flowering;  
XX transgenic plant; ss.  
OS Arabidopsis thaliana ecotype Columbia.  
XX  
FH Key Location/Qualifiers  
FT CDS 238..2064  
FT /\*tag= a  
XX WO9848007-A1.  
XX 29-OCT-1998.  
XX 17-APR-1998; 98WO-US07693.  
XX 18-APR-1997; 97US-0843572.  
XX (REGC ) UNIV CALIFORNIA.  
XX WPI; 1998-583656/49.  
XX P-PSDB; AAW79280.  
PT Alteration of plant circadian rhythms - by transformation with a  
PT transcription factor for the promoter of the Arabidopsis chlorophyll  
PT binding protein  
XX  
PS Claim 1; Page 43-47; 47pp; English.  
XX  
CC This cDNA sequence codes for a phytochrome-regulated transcription  
CC factor, designated CCA1 (see AAW79280), that binds to the promoter  
CC region of the chlorophyll binding protein gene (Lhcb1\*3) of  
CC Arabidopsis thaliana. To isolate the clone, a directional cDNA  
CC expression library was constructed in lambda gt22A using cDNA  
CC derived from leaves of Arabidopsis that had been grown in  
CC continuous white light for 3 weeks. The library was screened with  
CC an A2 fragment of the Lhcb1\*3 promoter. Overlapping phage clones  
CC provided a partial sequence, and the entire 5' end was determined  
CC by primer extension analysis. The CCA1 cDNA was subsequently used  
CC to identify a genomic clone (see AAV65381). A claimed method for  
CC altering plant response to daylength comprises transforming a plant  
CC with either the CCA1 genomic DNA or cDNA, a hybridizing sequence or  
CC a nucleic acid encoding a protein containing amino acids 24-75 of  
CC the 608-amino acid CCA1 protein. Manipulation of plant circadian  
CC rhythms (e.g. by overexpression of CCA1) can be used to delay  
CC flowering, and thus increase yield from both forage crops, where  
CC biomass will be produced for longer, and from seed crops such as  
CC rape, where a longer time in vegetative state will lead to larger  
CC plants and thus a higher seed set (claimed).  
XX  
SQ Sequence 2254 BP; 699 A; 473 C; 477 G; 605 T; 0 other;

Query Match 35.2%; Score 1527.6; DB 19; Length 2254;  
Best Local Similarity 87.9%; Pred. No. 0;  
Matches 1803; Conservative 0; Mismatches 9; Indels 240; Gaps 3;  
QY 2180 TCTCTCTCAGGTAGAGAGAGGCTGAAGCTAAAGGTGTAGCTATGGGTCAAGCGCTAGA 2239  
DB 441 TTTCTCCAAGGTAGAGAGAGGCTGAAGCTAAAGGTGTAGCTATGGGTCAAGCGCTAGA 500



Qy	2240	CATAGCTATTCTCTCCACGGCTTAAGCGTAAGCAAAACAATCCTTATCTCTCGAAAGAC	2299
Ds	501	CATAGCTATTCTCTCCACGGCTTAAGCGTAAGCAAAACAATCCTTATCTCTCGAAAGAC	560
Qy	2300	GGGAAGTGGAAACGATCCTTATGTCAAAAAACGGGTGTGAATCATGAAAGAGTCCCTTGG	2359
Ds	561	GGGAAGTGGAAACGATCCTTATGTCAAAAAACGGGTGTGAATCATGAAAGAGTCCCTTGG	620
Qy	2360	ATCAGAAAAAGTGTGCGATCCTCGAGGTGATTTTCATGGTCATATGGCATCTTTTTCAGT	2419
Ds	621	ATCAGAAAAAGTGTGCGATCCTCGAGGTGATTTTCATGGTCATATGGCATCTTTTTCAGT	643
Qy	2420	GTGTACATCTCTCTCATGTTATTAAATACAGATTGTGTCTTTCGTTTATAGATGGCCAA	2479
Ds	644	GTGTACATCTCTCTCATGTTATTAAATACAGATTGTGTCTTTCGTTTATAGATGGCCAA	653
Qy	2480	TGAAGATCGCAACAAATCAAAAGCCTGAAGAGAAACTCTGCAGGAAGACAATCTGTTCAGA	2539
Ds	654	TGAAGATCGCAACAAATCAAAAGCCTGAAGAGAAACTCTGCAGGAAGACAATCTGTTCAGA	713
Qy	2540	TTGTTTCACTCATCAGTATCTCTCTGTGCAATCTCTCCATGAATAAAAGTTGTATAGAGAC	2599
Ds	714	TTGTTTCACTCATCAGTATCTCTCTGTGCAATCTCTCCATGAATAAAAGTTGTATAGAGAC	773
Qy	2600	ATCAACGCAAGCACTTTCCGGAGTCTTCCGCTTCACGGGAAGAGTAAAAAAACAATCT	2659
Ds	774	ATCAACGCAAGCACTTTCCGGAGTCTTCCGCTTCACGGGAAGAGTAAAAAAACAATCT	817
Qy	2660	TTTATTTGCTATTTGAGGTTTTTAAGACGATTAGTACTTTTTCATGAACCTAAACACGTTGGG	2719
Ds	818	TTTATTTGCTATTTGAGGTTTTTAAGACGATTAGTACTTTTTCATGAACCTAAACACGTTGGG	817
Qy	2720	GAATTAACAGGGAATCAGAAATAACAGGTAAGAAAGAGTCAAACTCAGATTTTGAATGCA	2779
Ds	818	GAATTAACAGGGAATCAGAAATAACAGGTAAGAAAGAGTCAAACTCAGATTTTGAATGCA	870
Qy	2780	AAATCTCTGGAACAGGTAATGACCAAGGAGTCAAGTATTCAGATCATATCCCTGTG	2839
Ds	871	AAATCTCTGGAACAGGTAATGACCAAGGAGTCAAGTATTCAGATCATATCCCTGTG	930
Qy	2840	CTAGTGCCATTTGGGAGCTCAATAACAAAGTTCTCTATCACATCTCTCTTCAGAGCCAGAT	2899
Ds	931	CTAGTGCCATTTGGGAGCTCAATAACAAAGTTCTCTATCACATCTCTCTTCAGAGCCAGAT	990
Qy	2900	AGTCATCCCCACACAGTTGCGAGGATTAATCAGTCTGTTTCTTAATCATATAATGTCAACC	2959
Ds	991	AGTCATCCCCACACAGTTGCGAGGATTAATCAGTCTGTTTCTTAATCATATAATGTCAACC	1050
Qy	2960	CTTTTACAAACACGGCTCTTATCTGCGCAACTTTCGCTCATCATTTTGGCCTCCC	3019
Ds	1051	CTTTTACAAACACGGCTCTTATCTGCGCAACTTTCGCTCATCATTTTGGCCTCCC	1110
Qy	3020	GATTCTAGTGTGCTCACCTGTTTCCAGGGAATCACTCCGAATCTGGCTGCCATGGCC	3079
Ds	1111	GATTCTAGTGTGCTCACCTGTTTCCAGGGAATCACTCCGAATCTGGCTGCCATGGCC	1170
Qy	3080	GCAGCCACTGTGTGAGTGTGCTGTGTGGCTGCCAATGGAATTAACCTTTATGT	3139
Ds	1171	GCAGCCACTGTGTGAGTGTGCTGTGTGGCTGCCAATGGAATTAACCTTTATGT	1230
Qy	3140	GCTCTCTTAGTGTGAGTGTGCTGTGTGGCTGCCAATGGAATTAACCTTTATGT	3199
Ds	1231	GCTCTCTTAGTGTGAGTGTGCTGTGTGGCTGCCAATGGAATTAACCTTTATGT	1290
Qy	3200	GATGTAGATACAAAGCAAGCACTTTTCAACATGTTCTGTGCGAGCCGAGAGCAA	3259
Ds	1291	GATGTAGATACAAAGCAAGCACTTTTCAACATGTTCTGTGCGAGCCGAGAGCAA	1350
Qy	3260	GAACACTCCGAGGCATCAAAAGGCTCGATCTTCTACTGGACTCAGAGGATGTTGAAAAAAG	3319
Ds	1351	GAACACTCCGAGGCATCAAAAGGCTCGATCTTCTACTGGACTCAGAGGATGTTGAAAAAAG	1410

RESULT 3

AAD06664

ID AAD06664 standard; cDNA; 2240 BP.

XX AAD06664;

XX AC

XX AC

DT 10-AUG-2001 (first entry)

XX

Qy	3320	AGTAAACGAGTTTCTCATGAGCAGCCTTCTGCAACACCTGAGAGTGATGCAAAAGGGTTCA	3379
Ds	1411	AGTAAACGAGTTTCTCATGAGCAGCCTTCTGCAACACCTGAGAGTGATGCAAAAGGGTTCA	1470
Qy	3380	GATCGAGCAGGACAGAAAACAAGTTGACCGGTCTCTGCTGGCTCAACACACTCCGTCG	3439
Ds	1471	GATCGAGCAGGACAGAAAACAAGTTGACCGGTCTCTGCTGGCTCAACACACTCCGTCG	1530
Qy	3440	AGTAGTGATGTTGTAGGGCGATGCATCAAGAAAGGCAAGAGGATGGCACCACCAATGGTGA	3499
Ds	1531	AGTAGTGATGTTGTAGGGCGATGCATCAAGAAAGGCAAGAGGATGGCACCACCAATGGTGA	1590
Qy	3500	GTGAAAGAAACGAATGAAGACACTAATAAACCCTCAAACCTCAGAGTCCAAATGCGACCGCC	3559
Ds	1591	GTGAAAGAAACGAATGAAGACACTAATAAACCCTCAAACCTCAGAGTCCAAATGCGACCGCC	1650
Qy	3560	AGTAGAATCAGCTCCAATATAAACCAGTCCATGGAAGTCTGCTGACGAGGTACTTACT	3619
Ds	1651	AGTAGAATCAGCTCCAATATAAACCAGTCCATGGAAGTCTGCTGCTGACGAGGTACTTACT	1700
Qy	3620	TGGAATAAGATCAACTTCTTTTATTTTCAATCATTTTCTCATATAAATATTGTACATTC	3679
Ds	1701	TGGAATAAGATCAACTTCTTTTATTTTCAATCATTTTCTCATATAAATATTGTACATTC	1700
Qy	3680	GGTTCGAATTCCTTCCAAAGCTCTCTTCTCAGAGAGGTATTCGCCGCAAGTTTACATA	3739
Ds	1701	GGTTCGAATTCCTTCCAAAGCTCTCTTCTCAGAGAGGTATTCGCCGCAAGTTTACATA	1760
Qy	3740	TCGAGAGAACACACAGAGAGGAGAACACACACACACACACACACACACACACACACAC	3799
Ds	1761	TCGAGAGAACACACAGAGAGGAGAACACACACACACACACACACACACACACACACAC	1820
Qy	3800	TGATCTTAACTTCAACAGCTCAGTTTAAACACACAGTTTGTATGATCAAGAGGAGAGAGAACAC	3859
Ds	1821	TGATCTTAACTTCAACAGCTCAGTTTAAACACACAGTTTGTATGATCAAGAGGAGAGAGAACAC	1880
Qy	3860	AGGATTTCTTGGAAATCGGATTTAGATGCTTCAAAGCTTAAAGTATAGAGGAGAACAGGTTT	3919
Ds	1881	AGGATTTCTTGGAAATCGGATTTAGATGCTTCAAAGCTTAAAGTATAGAGGAGAACAGGTTT	1940
Qy	3920	TAAACCATACAAAGATGTTCCATGGAAGCCAAAGAAAGTAAATCTTCAACACCAATCC	3979
Ds	1941	TAAACCATACAAAGATGTTCCATGGAAGCCAAAGAAAGTAAATCTTCAACACCAATCC	2000
Qy	3980	TATCATTTATGTAACAGAAAGATCCAAACGATCGGTTGGAACTCAAGCTTCCAC	4039
Ds	2001	TATCATTTATGTAACAGAAAGATCCAAACGATCGGTTGGAACTCAAGCTTCCAC	2060
Qy	4040	ATGAGACTCTATTTTCACTGATCTGTGTGTTGTTGTTGTTTAAAGTTTCAAGACCA	4099
Ds	2061	ATGAGACTCTATTTTCACTGATCTGTGTGTTGTTGTTGTTTAAAGTTTCAAGACCA	2120
Qy	4100	CTGCTACATTTCTTTTCTTTTTCAGGCGCTTGTATTTGTTTCTTGTGCTTGTCTTCC	4159
Ds	2121	CTGCTACATTTCTTTTCTTTTTCAGGCGCTTGTATTTGTTTCTTGTGCTTGTCTTCC	2180
Qy	4160	TGTAACATTTGACTCTCTTATTATTCAACAAATCATAACTGTTTAACTTTTTTTTCCCA	4219
Ds	2181	TGTAACATTTGACTCTCTTATTATTCAACAAATCATAACTGTTTAACTTTTTTTTCCCA	4240
Qy	4220	ACCTGGAAGAA 4231	
Ds	2241	AAAAAAAAAAAA 2252	

DE A. thaliana transcription factor G680 homolog, G214 cDNA.

XX Plant transcription factor; phenotype; sugar sensing characteristic;  
 KW transgenic plant; plant yield; growth; germination; photosynthesis;  
 KW glyoxylate metabolism; respiration; pathogen response; wounding response;  
 KW cell cycle regulation; pigmentation; flowering; senescence; physiology;  
 KW storage organ; metabolism; ss.

OS Arabidopsis thaliana.

XX Key Location/Qualifiers

PH CDS 238..2064

FT /tag= a

FT /product= "Transcription factor homolog"

XX WO200135725-A1.

XX 25-MAY-2001.

XX 14-NOV-2000; 2000WO-US31414.

XX 17-NOV-1999; 99US-0166228.

PR 17-APR-2000; 2000US-0197899.

PR 22-AUG-2000; 2000US-0227439.

XX (MEND-) MENDEL BIOTECHNOLOGY INC.

PA (JIAN/) JIANG C.

PA (HEAR/) HEARD J.

PA (PINE/) PINEDA O.

PA (PILG/) PILGRIM M.

PA (ADAM/) ADAM L.

PA (RIEC/) RIECHMANN J L.

PA (YUGG/) YU G.

PA (SAMA/) SAMAH R.

XX Jiang C, Heard J, Pineda O, Pilgrim M, Adam L, Riechmann JI;

PI Yu G, Samaha R;

XX WPI; 2001-335977/35.

DR P-PSDB; AAE02563.

XX Nucleic acids encoding plant transcription factor polypeptides, useful  
 PT for altering the sugar sensing characteristics of plants and increasing  
 PT yield, e.g. corn, potato and cotton plants -

XX Claim 4; Page 122-124; 15pp; English.

XX The patent relates to polynucleotides encoding 35 plant transcription  
 CC factors which may be used to modify phenotype associated with a plant's  
 CC sugar sensing characteristics and increasing yield when their expression  
 CC level is altered. Sugars are central regulatory molecules that control  
 CC aspects of physiology, metabolism and development. Therefore the cDNAs  
 CC and proteins of the invention are useful for modifying the growth and  
 CC germination rates of plants, photosynthesis, glyoxylate metabolism,  
 CC respiration, starch and sucrose synthesis and degradation, pathogen  
 CC response, wounding response, cell cycle regulation, pigmentation,  
 CC flowering and senescence of plants and for modifying sink-source  
 CC relationships in seeds, tubers, roots, and other storage organs leading  
 CC to an increase in yield. The transcription factor polynucleotides and  
 CC polypeptides may be used to alter the structure and developmental  
 CC characteristics of plants such as soybean, wheat, corn, potato, cotton,  
 CC rice, oilseed, sunflower, alfalfa, sugarcane, turf, banana, blackberry,  
 CC blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower,  
 CC coffee, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon,  
 CC onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn,  
 CC tobacco, tomato, watermelon, roseaceous fruits and/or vegetable brassicas.  
 CC The present sequence is a homolog of Arabidopsis thaliana transcription  
 CC factor cDNA.

XX Sequence 2240 BP; 685 A; 473 C; 477 G; 605 T; 0 other;

XX Query Match

XX Best Local Similarity 35.1%; Score 1525.2; DB 22; Length 2240;

XX 88.1%; Pred. No. 0;

	Matches	1797;	Conservative	0;	Mismatches	3;	Indels	240;	Gaps	3;
OY	2180	TCTCTCTCAGGTAGAGAGAGAGGCTGAAGCTTAAGGTGTAGCTATATGGTCAAGCGCTAGA	2239							
DB	441	TTTCTCCAAGGTAGAGAGAGAGGCTGAAGCTTAAGGTGTAGCTATATGGTCAAGCGCTAGA	500							
OY	2240	CATAGCTATTCTCTCCACGCGCTTAAGCGTAAACCAACAATCTTATCTCTCGAAGAC	2299							
DB	501	CATAGCTATTCTCTCTCCACGCGCTTAAGCGTAAACCAACAATCTTATCTCTCGAAGAC	560							
OY	2300	GGGAAGTGGAAACGATCTTATGTCAAAAACGGGTGTGAATGATGAAAGAGTCCCTTGG	2359							
DB	561	GGGAAGTGGAAACGATCTTATGTCAAAAACGGGTGTGAATGATGAAAGAGTCCCTTGG	620							
OY	2360	ATCAGAAAAAGTGTGCGCATCTCTGAGGTGATTTTCATGGTTCATATGGCATCTTTTTCAGT	2419							
DB	621	ATCAGAAAAAGTGTGCGCATCTCTGAGGTGATTTTCATGGTTCATATGGCATCTTTTTCAGT	643							
OY	2420	GTGTACATTCCTCTCATGTTTATTAATACAGATTGTGTGCTTCGTTTATAGATGCCAA	2479							
DB	644	GTGTACATTCCTCTCATGTTTATTAATACAGATTGTGTGCTTCGTTTATAGATGCCAA	653							
OY	2480	TGAAGATCGAACCAATCAAAAGCCTGAAGAGAAAACTCTGCAAGGAAGACAATCTGTTCAGA	2539							
DB	654	TGAAGATCGAACCAATCAAAAGCCTGAAGAGAAAACTCTGCAAGGAAGACAATCTGTTCAGA	713							
OY	2540	TTGTTTCACTCATCAGTATCTCTGCTGTCATCTCTCCATGAATAAAGTTGTATAGAGAC	2599							
DB	714	TTGTTTCACTCATCAGTATCTCTGCTGTCATCTCTCCATGAATAAAGTTGTATAGAGAC	773							
OY	2600	ATCAAAACGAAGCACTTTCCGCGAGTTCTTCCCTTTCAGCGGAAGAGGTAAAAACAATCT	2659							
DB	774	ATCAAAACGAAGCACTTTCCGCGAGTTCTTCCCTTTCAGCGGAAGAGGTAAAAACAATCT	817							
OY	2660	TTCAITGCTATTGAGGTTTTTAAGACGATGTAGTACTTTTCATGAAAACTAAAAACCGTGGG	2719							
DB	818	TTCAITGCTATTGAGGTTTTTAAGACGATGTAGTACTTTTCATGAAAACTAAAAACCGTGGG	817							
OY	2720	GAATAACAGGGAAGTTCAGAAATAACAGGGTAAGAAGGAGTCAAACTCAGATTTGAATGCA	2779							
DB	818	GAATAACAGGGAAGTTCAGAAATAACAGGGTAAGAAGGAGTCAAACTCAGATTTGAATGCA	870							
OY	2780	AAATCTCTGAAAAACGGTAATGAGCAAGGACCTCAGACTTATCCGATGCATATCCCTGTG	2839							
DB	871	AAATCTCTGAAAAACGGTAATGAGCAAGGACCTCAGACTTATCCGATGCATATCCCTGTG	930							
OY	2840	CTAGTGCCATTGGGGAGCTCAATTAACAAGTTCTCTATCACATCTCTTTCAGAGCCAGAT	2899							
DB	931	CTAGTGCCATTGGGGAGCTCAATTAACAAGTTCTCTATCACATCTCTTTCAGAGCCAGAT	990							
OY	2900	AGTCATCCCAACAGATTGCAAGGAGATTATCAGTCGTTTCTTCTATCATATATATGTCACCC	2959							
DB	991	AGTCATCCCAACAGATTGCAAGGAGATTATCAGTCGTTTCTTCTATCATATATATGTCACCC	1050							
OY	2960	CTTTTACAAACACCGGCTTTTATATCTGCCCAAACTTTTCGCTCATCATATTTTGGCTCCC	3019							
DB	1051	CTTTTACAAACACCGGCTTTTATATCTGCCCAAACTTTTCGCTCATCATATTTTGGCTCCC	1110							
OY	3020	GATTCTAGTGTGCTCACCTGTTCCAGGGAACCTCACCTCCGAATCTCGGTGCCATGCC	3079							
DB	1111	GATTCTAGTGTGCTCACCTGTTCCAGGGAACCTCACCTCCGAATCTCGGTGCCATGCC	1170							
OY	3080	GCAGCCACTGTTGAGCTGTAGTGTGTTGGGGCTGCCAATGGATTATACCTTTTATGT	3139							
DB	1171	GCAGCCACTGTTGAGCTGTAGTGTGTTGGGGCTGCCAATGGATTATACCTTTTATGT	1230							
OY	3140	GCTCCTCTTAGTTCAGTGGTTTTCACATAGTCATCTCCATCTACTTTTGGACCATCATGT	3199							
DB	1231	GCTCCTCTTAGTTCAGTGGTTTTCACATAGTCATCTCCATCTACTTTTGGACCATCATGT	1290							
OY	3200	GATGTAGATACAAAAAGCAAGCACTTTTACAAATGGTTCTGTGCAGAGCCGAGAGCAA	3259							
DB	1291	GATGTAGATACAAAAAGCAAGCACTTTTACAAATGGTTCTGTGCAGAGCCGAGAGCAA	1350							





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XX FH Key Location/Qualifiers
FT CDS 238..2064
FT FT /*tag= a
FT FT /product= "Transcription factor, G214"
XX PN WO200136597-A1.
XX PD 25-MAY-2001.
XX PF 14-NOV-2000; 2000WO-US31344.
XX PR 17-NOV-1999; 99US-0166228.
XX PR 17-APR-2000; 2000US-0197899.
XX PR 22-AUG-2000; 2000US-0227439.
XX PA (MEND-) MENDEL BIOTECHNOLOGY INC.
XX PA (CREE/) CREELMAN R.
XX PA (YUGG/) YU G.
XX PA (ADAM/) ADAM L.
XX PA (RIEC/) RIECHMANN J L.
XX PA (HEAR/) HEARD J.
XX PA (SAMA/) SAMAHA R.
XX PA (PILG/) PILGRIM M.
XX PA (PINE/) PINEDA O.
XX PA (JIANG/) JIANG C.
XX PI Creelman R, Yu G, Adam L, Riechmann JL, Heard J, Samaha R;
XX PI Pilgrim M, Pineda O, Jiang C;
XX DR WPI: 2001-335999/35.
XX DR P-PSDB; AAE01889.
XX PT Nucleic acids encoding plant transcription factor polypeptides, useful
XX PT for altering the biochemical characteristics of plants e.g. corn,
XX PT potato and cotton plants -
XX PS Claim 4; Page 55-57; 127pp; English.
XX CC The present sequence is Arabidopsis thaliana transcription factor,
XX CC G214 cDNA. The transcription factor is used for altering a plant's
XX CC biochemical characteristics. The transcription factor may be used to
XX CC alter the structure and developmental characteristics of plants such as
XX CC soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower,
XX CC alfalfa, sugar cane, turf, banana, blackberry, blueberry, strawberry,
XX CC raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant,
XX CC grapes, honey dew, lettuce, mango, melon, onion, papaya, peas, peppers,
XX CC pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon,
XX CC rosaceous fruits and/or vegetable brassicas. Transcription factors are
XX CC key controlling elements of biological pathways and altering expression
XX CC levels of 1 or more transcription factors can change entire biological
XX CC pathways in an organism. Therefore manipulating transcription factor
XX CC levels in plants offers great potential in agricultural biotechnology
XX CC for modifying a plant's traits. Transcription factor cDNA is useful in
XX CC gene therapy.
XX SQ Sequence 2240 BP; 685 A; 473 C; 477 G; 605 T; 0 other;

Query Match 35.1%; Score 1525.2; DB 22; Length 2240;
Best Local Similarity 88.1%; Pred. No. 0;
Matches 1797; Conservative 0; Mismatches 3; Indels 240; Gaps 3;

QY 2180 TCTCTCAGGTAGAGAAAGAGGCTGAAGCTAAAGGTAGCTATGGGTCAAGCGCTAGA 2239
DB 441 TTTCTCAAAGTAGAGAAAGAGGCTGAAGCTAAAGGTAGCTATGGGTCAAGCGCTAGA 500
QY 2240 CATAGCTATTCCTCCACGGCTAAGGCTAAACCAACATCCTATCCTCGAAGAC 2299
DB 501 CATAGCTATTCCTCCACGGCTAAGGCTAAACCAACATCCTATCCTCGAAGAC 560
QY 2300 GGGAGGTGAACGATCCTTATGTCAAAAAACGGGTGTGAATGATGGAAGAGTCCCTCG 2359
DB 561 GGGAGGTGAACGATCCTTATGTCAAAAAACGGGTGTGAATGATGGAAGAGTCCCTCG 620

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QY 2360 ATCAGAAAAAGTGTGCGATCCTGAGGTGATTTTTCATGTCATATGCGATCTTTTTCAGT 2419
DB 621 ATCAGAAAAAGTGTGCGATCCTG----- 643
QY 2420 GTGTCAATTCCTCCTCATGTTTAAATACAGATTTGTGCTTCGTTTATAGATGGCAA 2479
DB 644 -----AGATGGCAA 653
QY 2480 TGAAGATCGACAACAATCAAAGCCTGAAGAGAAAACTCTCAGGAGACAACTCTTCAGA 2539
DB 654 TGAAGATCGACAACAATCAAAGCCTGAAGAGAAAACTCTCAGGAGACAACTCTTCAGA 713
QY 2540 TTGTTTCACTCATCAGTATCTCTCTGCTGATCCTCCATCAATAAAAAAGTTGTATAGAGAC 2599
DB 714 TTGTTTCACTCATCAGTATCTCTCTGCTGATCCTCCATCAATAAAAAAGTTGTATAGAGAC 773
QY 2600 ATCAAAACGAAGCATTTCGCGAGTCTTTGCGCTTCAACGGAAGAGGTAAAAACAATCT 2659
DB 774 ATCAAAACGAAGCATTTCGCGAGTCTTTGCGCTTCAACGGAAG----- 817
QY 2660 TTCAATTGCTATTGAGGTTTAAAGACGATTAGTACTTTTTCATGAAACTAAAAACGTCGGG 2719
DB 818 ----- 817
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DB 1824 ATGA 1827

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ID ABZ16387 standard; DNA; 1134 BP.  
XX AC ABZ16387;  
XX AC  
XX 21-JAN-2003 (first entry)  
XX XX  
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 4192.  
XX XX  
KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.  
XX XX  
OS Arabidopsis thaliana.  
XX XX  
PN WO200216655-A2.  
XX XX  
PD 28-FEB-2002.  
XX XX  
PF 24-AUG-2001; 2001WO-US26685.  
XX XX  
PR 24-AUG-2000; 2000US-227866P.  
PR 26-JAN-2001; 2001US-264647P.  
PR 22-JUN-2001; 2001US-300111P.  
XX XX  
PA (SCRI ) SCRIPPS RES INST.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX XX  
PI Harper JF, Kreps J, Wang X, Zhu T;  
XX XX  
WPI; 2002-304127/34.  
XX XX  
PT Identifying a stress condition to which a plant cell has been exposed  
and producing plants with increased tolerance to these abiotic stresses  
- .  
PS Claim 144; SEQ ID NO 4192; 577pp + Sequence Listing; English.  
XX XX  
CC The invention relates to identifying a stress condition to which a plant  
cell has been exposed, comprising:  
CC (a) contacting nucleic acid representative of expressed polynucleotides  
in the plant cell with an array or probes representative of the plant  
cell genome; and  
CC (b) detecting a profile of expressed polynucleotides in the plant cell  
characteristic of a stress response. The method is useful in the  
CC production of transgenic plants, cells and seeds and in producing plants  
with increased tolerance to abiotic stress. The present sequence is that  
CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used  
in methods of the invention.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification but is based on sequence information supplied to Derwent by  
CC the European Patent Office.  
XX XX









RESULT 10  
AAC34359  
ID AAC34359 standard; DNA; 895 BP.  
XX AC AAC34359;  
XX DT 17-OCT-2000 (first entry)  
XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 6367.  
XX DE Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; es.  
XX OS Arabidopsis thaliana.  
XX PN EF1033405-A2.  
XX PD 06-SEP-2000.  
XX PF 25-FEB-2000; 2000EP-0301439.  
XX PR 25-FEB-1999; 99US-0121825.  
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Best Local Similarity 95.7%; Pred. No. 2.8e-63;
Matches 315; Conservative 0; Mismatches 14; Indels 0; Gaps 0
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Qy	234	AGGCCATTCATGAAATTTGGAATGMAAGGATATCAAAGAATCTTAACAAGGCCACGCTCT	293
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Qy	354	GGTCTTTTTTAGCTCAAAGTATCATGCCATTTATGTCAAAAGTGTGTGAATAATTCCTCAAGAC	413
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DT	18-OCT-2000 (first entry)
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DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 61192.
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KW	Hybridisation assay; genetic mapping; gene expression control;
KW	protein identification; signal transduction pathway;
KW	metabolic pathway; promoter; termination sequence; ss.
XX	
OS	Arabidopsis thaliana.
XX	
PN	EP1033405-A2.
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Query Match 7.0%; Score 304.6; DB 21; Length 844;  
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DT 18-OCT-2000 (first entry)
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
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Best Local Similarity 95.7%; Pred. No. 8.6e-63;
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Qy 414 TATATATGAGATGTTTGTGTTTCATTTT 440
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XX 18-OCT-2000 (first entry)
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XX KW Hybridisation assay; genetic mapping; gene expression control;
XX KW protein identification; signal transduction pathway;
XX KW metabolic pathway; promoter; termination sequence; ss.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
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XX PR 05-MAR-1999; 99US-0123180.
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Matches 125; Conservative

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KW protein identification; signal transduction pathway;	
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Total number of hits satisfying chosen parameters: 5105512

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	1827	81.1	1827	24	ABZ13695
6	1527.6	67.8	4344	19	AAV65381
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8	217.2	9.6	2526	22	AAV06648

9	217.2	9.6	2526	22	AAV05761
10	217.2	9.6	2526	22	AAV05787
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12	213	9.4	1938	24	ABZ13311
13	189	8.4	1134	24	ABZ16387
14	144.2	6.4	2730	21	AAV04080
15	118.8	5.3	364	21	AAV57320
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17	104.2	4.6	1148	21	AAV45095
18	103.2	4.6	1199	21	AAV49487
19	103	4.6	1166	22	AAV05830
20	103	4.6	1197	21	AAV38743
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23	97.2	4.3	1419	21	AAV36749
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25	92.4	4.1	919	21	AAV56354
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27	87.6	3.9	450	21	AAV57286
28	87.6	3.9	541	21	AAV56124
29	83.2	3.7	1612	21	AAV57364
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33	75.4	3.3	666	19	AAV09298
34	74.8	3.3	365	25	ABX18648
35	73.8	3.3	373	21	AAV56764
36	73	3.2	592	25	ABX56693
37	68	3.0	320	21	AAV56665
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#### ALIGNMENTS

#### RESULT 1

AAV65382

ID AAV65382 standard; cDNA to mRNA; 2254 BP.

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XX AC

XX AC

DT 15-FEB-1999 (first entry)

XX Arabidopsis phytochrome regulated transcription factor CCAL cDNA.

DE Arabidopsis phytochrome regulated transcription factor; CCAL.

XX Arabidopsis phytochrome regulated transcription factor; CCAL.

KW chlorophyll binding protein; Lhcb1\*3; circadian rhythm; flowering;

KW transgenic plant; ss.

XX Arabidopsis thaliana ecotype Columbia.

XX Arabidopsis thaliana ecotype Columbia.

PH Key

FT CDS

FT CDS

FT CDS

XX WO9848007-A1.

XX 29-OCT-1998.

XX 17-APR-1998; 98WO-US07693.

XX 18-APR-1997; 97US-0843572.

XX (REGC ) UNIV CALIFORNIA.

XX WPI; 1998-583656/49.

DR

DR P-PSDB; AAW9280.  
XX Alteration of plant circadian rhythms - by transformation with a  
PT transcription factor for the promoter of the Arabidopsis chlorophyll  
PT binding protein  
XX  
PS Claim 1; Page 43-47; 47pp; English.  
XX  
CC This cDNA sequence codes for a phytochrome-regulated transcription  
CC factor, designated CCAL (see AAW9280), that binds to the promoter  
CC region of the chlorophyll binding protein gene (Lhcb1\*3) of  
CC Arabidopsis thaliana. To isolate the clone, a directional cDNA  
CC expression library was constructed in lambda gt22a using cDNA  
CC derived from leaves of Arabidopsis that had been grown in  
CC continuous white light for 3 weeks. The library was screened with  
CC an A2 fragment of the Lhcb1\*3 promoter. Overlapping phage clones  
CC provided a partial sequence, and the entire 5' end was determined  
CC by primer extension analysis. The CCAL cDNA was subsequently used  
CC to identify a genomic clone (see AAW65381). A claimed method for  
CC altering plant response to daylength comprises transforming a plant  
CC with either the CCAL genomic DNA or cDNA, a hybridising sequence or  
CC a nucleic acid encoding a protein containing amino acids 24-75 of  
CC the 608-amino acid CCAL protein. Manipulation of plant circadian  
CC rhythms (e.g. by overexpression of CCAL) can be used to delay  
CC flowering, and thus increase yield from both forage crops, where  
CC biomass will be produced for longer, and from seed crops such as  
CC rape, where a longer time in vegetative state will lead to larger  
CC plants and thus a higher seed set (claimed).  
XX  
SQ Sequence 2254 BP; 699 A; 473 C; 477 G; 605 T; 0 other;

Query Match 100.0%; Score 2254; DB 19; Length 2254;  
Best Local Similarity 100.0%; Pred. No. 0;  
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QY 181 TCTCTAAAGTGGAAATTTTGTAAAGAGAAAGATCTGAAGTCTGAGAGGCTTAGTGATG 240  
DB 181 TCTCTAAAGTGGAAATTTTGTAAAGAGAAAGATCTGAAGTCTGAGAGGCTTAGTGATG 240  
QY 241 GAGACAAATTCGTCTGAGAGATCTCGTTATTAAAGACTCGGAAGCCATATACGATAACA 300  
DB 241 GAGACAAATTCGTCTGAGAGATCTCGTTATTAAAGACTCGGAAGCCATATACGATAACA 300  
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DB 301 AAGCAAGCTCAAGGTCGACTGAGGAGAACATTAATAGATTTCATTGAAGCTTTGAGGCTT 360  
QY 361 TATGGTAGACATGGCAGAGAGATTGAAGAACATCTAGCAACAAACCTGCTGCCAGATA 420  
DB 361 TATGGTAGACATGGCAGAGAGATTGAAGAACATCTAGCAACAAACCTGCTGCCAGATA 420  
QY 421 AGAAGTCACGCTCAGAAATTTTCTCCAAAGTAGAGAGAGGCTGAAGCTAAAGGTGTA 480  
DB 421 AGAAGTCACGCTCAGAAATTTTCTCCAAAGTAGAGAGAGGCTGAAGCTAAAGGTGTA 480  
QY 481 GCTATGGTCAAGGCTAGACATAGCTATTCTCTCCAGGCTTAAGCGTAAACCAAC 540  
DB 481 GCTATGGTCAAGGCTAGACATAGCTATTCTCTCCAGGCTTAAGCGTAAACCAAC 540  
QY 541 AATCCCTTATCTCGAAAGACGGGAAGTGGAAACGATCTTATGTCAAAACCGGTGTAAT 600  
DB 541 AATCCCTTATCTCGAAAGACGGGAAGTGGAAACGATCTTATGTCAAAACCGGTGTAAT 600

DB 541 AATCCCTTATCTCGAAAGACGGGAAGTGGAAACGATCTTATGTCAAAACCGGTGTAAT 600  
QY 601 GATGGAAGAGAGTCCCTTGGATCAGAAAAAGTGTCCGATCTGAGATGGCCAAATGAAGAT 660  
DB 601 GATGGAAGAGAGTCCCTTGGATCAGAAAAAGTGTCCGATCTGAGATGGCCAAATGAAGAT 660  
QY 661 CGAACAAATCAAGAGCTGAAGAGAAAACTCTGAGGAAGACAACTGTTCAGATTTGTTTC 720  
DB 661 CGAACAAATCAAGAGCTGAAGAGAAAACTCTGAGGAAGACAACTGTTCAGATTTGTTTC 720  
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DB 721 ACTCATCAGTATCTCTCTGTCGATCTCTCCATGAATAAAGTTGTATAGACATCAAAAC 780  
QY 781 GCAAGCACTTTCCGCGAGTCTTCCCTTACGGGAAGGGAAGTGCAGAAATACAGGGTA 840  
DB 781 GCAAGCACTTTCCGCGAGTCTTCCCTTACGGGAAGGGAAGTGCAGAAATACAGGGTA 840  
QY 841 AGAAGAGAGTCAAACTCAGATTTGAATGCAAAATCTCTGGAACCGGTAATGAGCAAGCA 900  
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DB 1021 CAGTCTGTTTCTTAATCATATAATGTCAAACCTTTTACAAACACCGGCTCTTTTACTGCC 1080  
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DB 1321 CAACATGGTTCTGTGACAGCCGAGAGCAAGAACACTCCGAGGCTCAAAAGGCTCGATCT 1380  
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DB 1381 TCATCGACTCAGAGGATTTGAAAAATAGAGTAAACAGTTCATAGCAGCCTTCT 1440  
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DB 1441 GCAACACCTCAGAGTGTGCAAAAGGTTTCTAGTGGAGCAGAGACAGAAACAAAGTTGAC 1500  
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DB 1501 CGGTCTCTGTGCTCAAAACCTCCGTCCAGTGTGATGATGTTGAGGCGGATGCATCA 1560  
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DB 1621 CCTCAAACTTCAGAGTCCCAATGACCGCGCAGTGTAGATTCAGTCCCAATTAACCGATCCA 1680









13261	Db	CATCCTCCATCTACTTTTGGACCAATCATGTGATGTAGAGTACACAAAGCAAGCACTTTA	13262
1321	Qy	CAACATGGTTCTGTGCAGAGCCGAGAGCAAGAAACACTCCGAGGCATCAAAAGGCTCGATCT	13263
1321	Db	CAACATGGTTCTGTGCAGAGCCGAGAGCAAGAAACACTCCGAGGCATCAAAAGGCTCGATCT	13264
1381	Qy	TCACTGACTCAGAGGATGTTTGAAAATAAGAGTAAACAGTTTGTCTATGAGCAGCCTTCT	13265
1381	Db	TCACTGACTCAGAGGATGTTTGAAAATAAGAGTAAACAGTTTGTCTATGAGCAGCCTTCT	13266
1441	Qy	GCAACACCTCAGAGTGATGCAAGGGTTTCAGATGCGACGAGAGACAGAAACAGTTTGAC	13267
1441	Db	GCAACACCTCAGAGTGATGCAAGGGTTTCAGATGCGACGAGAGACAGAAACAGTTTGAC	13268
1501	Qy	CGGTCTCTGTGGCTCAAAACACTCCGTGCAGTAGTGATGTTGAGGCGGATGCATCA	13269
1501	Db	CGGTCTCTGTGGCTCAAAACACTCCGTGCAGTAGTGATGTTGAGGCGGATGCATCA	13270
1561	Qy	GAAGGCAAGAGGATGGCACCAATGTGTGAGGTGAAAGAAACGAATGAAGACACTAATAAA	13271
1561	Db	GAAGGCAAGAGGATGGCACCAATGTGTGAGGTGAAAGAAACGAATGAAGACACTAATAAA	13272
1621	Qy	CCTCAAACTTCAGAGTCCAAATGCAACGCGCAGTAGAATCAGTCCCAATATAACCGATCCA	13273
1621	Db	CCTCAAACTTCAGAGTCCAAATGCAACGCGCAGTAGAATCAGTCCCAATATAACCGATCCA	13274
1681	Qy	TGGAAGTCTGTGTCGACGAGGGTCGAAATGCGCTTCCAAGCTCTCTTCTCCAGAGAGGTA	13275
1681	Db	TGGAAGTCTGTGTCGACGAGGGTCGAAATGCGCTTCCAAGCTCTCTTCTCCAGAGAGGTA	13276
1741	Qy	TTGCCGCAAGTTTTACATATCGAGAGAACAACAGAGAGGAAGAAACAACAACAAGAA	13277
1741	Db	TTGCCGCAAGTTTTACATATCGAGAGAACAACAGAGAGGAAGAAACAACAACAAGAA	13278
1801	Qy	CAAGAATATCCAATGGCACTTGATCTTTAACTTCACAGCTCAGTTTAACACAGTTGATGAT	13279
1801	Db	CAAGAATATCCAATGGCACTTGATCTTTAACTTCACAGCTCAGTTTAACACAGTTGATGAT	13280
1861	Qy	CAAGAGAGAGAGAAACACAGGATTTCTTTGGAATCGGATTTAGATGTTCCAAAGCTAATG	13281
1861	Db	CAAGAGAGAGAGAAACACAGGATTTCTTTGGAATCGGATTTAGATGTTCCAAAGCTAATG	13282
1921	Qy	AGTAGAGGAAGAACAGGTTTTTAACCATACAAAAGATGTTCCATGGGAAGCCAAAGAAAGT	13283
1921	Db	AGTAGAGGAAGAACAGGTTTTTAACCATACAAAAGATGTTCCATGGGAAGCCAAAGAAAGT	13284
1981	Qy	AGAACTCTCAACAACAATCCTATCATTCATGTGGAACAGAAAGATCCCAACCGATGCGG	13285
1981	Db	AGAACTCTCAACAACAATCCTATCATTCATGTGGAACAGAAAGATCCCAACCGATGCGG	13286
2041	Qy	TTGGAAACTCAAGCTCCACATGAGACTCTATTTTCACTGATCTGTTGTTTCTACTCTG	13287
2041	Db	TTGGAAACTCAAGCTCCACATGAGACTCTATTTTCACTGATCTGTTGTTTCTACTCTG	13288
2101	Qy	TTTTTAAGTTTTCAAGACCACTGCTACATTTCTTTTTCTTTTGAGGCCCTTGATTTGT	13289
2101	Db	TTTTTAAGTTTTCAAGACCACTGCTACATTTCTTTTTCTTTTGAGGCCCTTGATTTGT	13290
2161	Qy	TTCTTGTCATAGTCTTCTGTGAACATTTTGACTCTGCTATTTATTTCAACAATCATAACT	13291
2161	Db	TTCTTGTCATAGTCTTCTGTGAACATTTTGACTCTGCTATTTATTTCAACAATCATAACT	13292
2221	Qy	GTTTAAATCTTTTTTTTTTCCA	2240
2221	Db	GTTTAAATCTTTTTTTTTTCCA	2240

## RESULT 4

RESULI 4  
AAD05773

ID AAD05773 standard; cDNA; 2240 BP.

XX

AC AAD05773;

XX  
XX  
15/150000

www

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Query Match      99.4%; Score 2240; DB 22; Length 2240;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 2240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAGATTTCCTCAATTCGCTAGCTTCGGTCTCTTTCTCTTTCTGTTTCATTGATCAAAAGCA 60
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[illegible]

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\_\_\_\_\_

Db 1 TGAGATTCTCCATTTCCGTTAGCTTCTGGTCTCTTTTCTTTGTTTTCATTGATCAAAAGCA 60  
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Db 61 AATCATTCTTCTTCTTCTTCTCTCGATTCTTTACTGTTTCTTATCCAAACGAAATCTG 120  
Qy 121 GAATTAATAAATGGAATCTTTATCGAATCCAAAGCTGATTTTGTCTTCTTCAATGAAATCATC 180  
Db 121 GAATTAATAAATGGAATCTTTATCGAATCCAAAGCTGATTTTGTCTTCTTCAATGAAATCATC 180  
Qy 181 TCTCTAAAGTGGAAATTTTGTAAAGAGAAAGATCTGAAGTGTGTAGAGGAGCTTAGTGATG 240  
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Qy 361 TATGGTAGACATGGCAGAAAGATTGAAAGAACATGTAGCAACAAAACTGCTGCCAGATA 420  
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Db 601 GATGGAAAGAGTCCCTTGGATCAGAAAAAGTGTGCGATCCTGAGATGGCCAATGAAGAT 660  
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Db 1801 CAAAGATATCCATGSCACTTGATCTTAACCTTCACAGCTCAGTTAAACACAGTTGATGAT 1860  
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Db 1861 CAAAGAGAGAGAGAGAAACACAGGATTTCTTGGAAATCGGATTTAGATGCTTCAAAAGCTAATG 1920  
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Oy 2221 GTTTAACTCTTTTTCCTCA 2240  
 Db |||||

## RESULT 5

ABZ13695  
 ID ABZ13695 standard; DNA; 1827 BP.

XX AC ABZ13695;  
 XX 21-JAN-2003 (first entry)  
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1500.  
 XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.  
 KW Arabidopsis thaliana.  
 XX Arabidopsis thaliana.

XX W0200216655-A2.

XX 28-FEB-2002.

XX 24-AUG-2001; 2001WO-US26685.

XX 24-AUG-2000; 2000US-227866P.

PR 26-JAN-2001; 2001US-264647P.

PR 22-JUN-2001; 2001US-300111P.

XX (SCRI ) SCRIPPS RES INST.

PA (SYGN ) SYNGENTA PARTICIPATIONS AG.

XX Harper JF, Kreps J, Wang X, Zhu T;

XX WPI; 2002-304127/34.

PT Identifying a stress condition to which a plant cell has been exposed  
 and producing plants with increased tolerance to these abiotic stresses

Claim 144; SEQ ID NO 1500; 577pp + Sequence Listing; English.

CC The invention relates to identifying a stress condition to which a plant  
 cell has been exposed, comprising:

CC (a) contacting nucleic acid representative of expressed polynucleotides  
 in the plant cell with an array or probes representative of the plant

CC cell genome; and

CC (b) detecting a profile of expressed polynucleotides in the plant cell

CC characteristic of a stress response. The method is useful in the

CC production of transgenic plants, cells and seeds and in producing plants  
 with increased tolerance to abiotic stress. The present sequence is that

CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used  
 in methods of the invention.

CC Note: The sequence data for this patent is not represented in the printed

CC specification but is based on sequence information supplied to Derwent by

CC the European Patent Office.

XX SQ Sequence 1827 BP; 591 A; 397 C; 419 G; 420 T; 0 other;

Query Match 81.1%; Score 1827; DB 24; Length 1827;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1827; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 238 ATGAGACAAATTCGTCTGGAGAAGATCTGGTTATTAAAGACTCGGAAGCCATATACGATA 297

Db 1 ATGAGACAAATTCGTCTGGAGAAGATCTGGTTATTAAAGACTCGGAAGCCATATACGATA 60

Oy 298 ACAAGCAAGCTGAAAGGTGGACTGAGGAAGACATAATAGATTCATTGAAGCTTTGAGG 357

Db 61 ACAAGCAAGCTGAAAGGTGGACTGAGGAAGACATAATAGATTCATTGAAGCTTTGAGG 120

Oy 358 CTTTATGGTAGACATGGCAGAGAGATTGAAGAACATGTACCAACAAACCTGCTGCCAG 417

|||

Db 121 CTTTATGGTAGACATGGCAGAGATTGAAGAACATGTAGCAACAAAACTGCTGTCAG 180  
 Oy 418 ATAGAAGTACGCTCAGAAATTTTCTCCAGGTAGAGAAGAGGCTGAAGCTTAAAGT 477  
 Db 181 ATAAGAAGTACGCTCAGAAATTTTCTCCAGGTAGAGAAGAGGCTGAAGCTTAAAGT 240  
 Oy 478 GTAGCTATGGTCAAGCGCTAGACATAGCTATTCTCTCTCCACGCGCTTAAGCGTAAACCA 537  
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 Db 721 AGTTCTCTATCACATCTCTTCAGAGCCAGATAGTATCCCCACACAGATTGCAGGAGAT 780  
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 Db 901 GGGAACTCAGCTCCGAACTCTGGTGGCATCGCCGACGACCACTGTTGAGCTGCTAGTGTCT 960  
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 Db 1081 TTCAACATGTTTCTGTGCAGAGCCGAGACGACGAACACTCCGAGGATCAAGAGCTCGA 1140  
 Oy 1378 TCTTCACTGGACTCAGAGGATGTTGAAAATAAGAGTAAACAGTTTGTGATGACAGCT 1437  
 Db 1141 TCTTCACTGGACTCAGAGGATGTTGAAAATAAGAGTAAACAGTTTGTGATGACAGCT 1200  
 Oy 1438 TCTGCAACCTCAGAGTGTATGCAAGGGTTTCAGATGGAGCAGGAGACGAAACCAAGTT 1497  
 Db 1201 TCTGCAACCTCAGAGTGTATGCAAGGGTTTCAGATGGAGCAGGAGACGAAACCAAGTT 1260

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 Db 1261 GACCGGTCTCGTGTGCTCAACACATCCGTCGAGTAGTGATGATGTTGAGCGGATGCA 1320  
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 Qy 1558 TCAGAAAGGCAAGAGGATGCGACCAATGGTGAGGTGAAGAAAGCAATGAAGACACTAAT 1617  
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 Db 1321 TCAGAAAGGCAAGAGGATGCGACCAATGGTGAGGTGAAGAAAGCAATGAAGACACTAAT 1380  
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 Qy 1618 AACCTCAAACTTCAGAGTCCAATGCAAGCGCAGTAGAATCAGCTCCAATATAACCGAT 1677  
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 Db 1381 AACCTCAAACTTCAGAGTCCAATGCAAGCGCAGTAGAATCAGCTCCAATATAACCGAT 1440  
 |  
 Qy 1678 CCATGGAAGTCTGTCTGACGAGGTGCAATGCTTCCAGCTCTCTCTCCAGAGAG 1737  
 |  
 Db 1441 CCATGGAAGTCTGTCTGACGAGGTGCAATGCTTCCAGCTCTCTCTCCAGAGAG 1500  
 |  
 Qy 1738 GTATTGCGCCAAAGTTTTACATATCGAGAGAACACAGAGAGGAGAACACACACAA 1797  
 |  
 Db 1501 GTATTGCGCCAAAGTTTTACATATCGAGAGAACACAGAGAGGAGAACACACACAA 1560  
 |  
 Qy 1798 GAACAAAGATATCCAATGGCACTTGATCTTTAACTTCAAGCTCAGTTAACACCACTTGAT 1857  
 |  
 Db 1561 GAACAAAGATATCCAATGGCACTTGATCTTTAACTTCAAGCTCAGTTAACACCACTTGAT 1620  
 |  
 Qy 1858 GATCAAGAGAGAGAGAGAAACACAGGATTTCTTGGAAATCGGATAGATGCTTCAAAGCTA 1917  
 |  
 Db 1621 GATCAAGAGAGAGAGAGAAACACAGGATTTCTTGGAAATCGGATAGATGCTTCAAAGCTA 1680  
 |  
 Qy 1918 ATCAGTAGAGAGAGAGAGAGGTTTTAAACCATACAGAAAGATGTTCCATGGAAGCCAAAGAA 1977  
 |  
 Db 1681 ATCAGTAGAGAGAGAGAGGTTTTAAACCATACAGAAAGATGTTCCATGGAAGCCAAAGAA 1740  
 |  
 Qy 1978 AGTAGAATCTCAACCAATCTCTATCATTCATGTTGGAACAGAAAGATCCCAACCGGATG 2037  
 |  
 Db 1741 AGTAGAATCTCAACCAATCTCTATCATTCATGTTGGAACAGAAAGATCCCAACCGGATG 1800  
 |  
 Qy 2038 CGGTTGGAAGTCAAGCTCCACATGA 2064  
 |  
 Db 1801 CGGTTGGAAGTCAAGCTCCACATGA 1827  
 |

## RESULT 6

AAV65381  
 ID AAV65381 standard; DNA; 4344 BP.

XX  
 AC AAV65381;

XX  
 DT 15-FEB-1999 (first entry)

XX Arabidopsis phytochrome regulated transcription factor CCA1 DNA.

KW Phytochrome regulated transcription factor; CCA1;  
 KW chlorophyll binding protein; Lhcb1\*3; circadian rhythm; flowering;  
 transgenic plant; ss.

XX Arabidopsis thaliana ecotype Columbia.

XX Key Location/Qualifiers

FT CDS 1332..4043

FT /tag= a

FT /note= "contains introns"

FT 1..1999

FT /tag= b

FT /number= 1

FT 1200..1283

FT /tag= c

FT /number= 1

FT 1332..1370

FT /tag= d

FT /number= 2

FT 1371..1448

FT /tag= e

FT exon /number= 2  
 1449..1560  
 /tag= f  
 FT intron /number= 3  
 1561..1648  
 /tag= g  
 FT exon /number= 3  
 1649..1710  
 /tag= h  
 FT intron /number= 4  
 1711..2189  
 /tag= i  
 FT exon /number= 4  
 2190..2384  
 /tag= j  
 FT intron /number= 5  
 2385..2471  
 /tag= k  
 FT exon /number= 5  
 2472..2645  
 /tag= l  
 FT intron /number= 6  
 2646..2728  
 /tag= m  
 FT exon /number= 6  
 2729..3610  
 /tag= n  
 FT intron /number= 7  
 3611..3680  
 /tag= o  
 FT exon /number= 7  
 3681..4043  
 /tag= p  
 /number= 8

WO9848007-A1.

XX 29-OCT-1998.

XX 17-APR-1998; 98WO-US07693.

XX 18-APR-1997; 97US-0843572.

XX (REGC ) UNIV CALIFORNIA.

XX WPI; 1998-583656/49.

XX P-PSDB; AAW79280.

XX Alteration of plant circadian rhythms - by transformation with a  
 transcription factor for the promoter of the Arabidopsis chlorophyll  
 binding protein

XX Claim 1; Page 36-40; 47pp; English.

XX This genomic DNA sequence codes for a phytochrome-regulated  
 transcription factor, designated CCA1 (see AAW79280), that binds to  
 the promoter region of the chlorophyll binding protein gene  
 (Lhcb1\*3) of Arabidopsis thaliana. The genomic clone was isolated  
 by screening an Arabidopsis ecotype Columbia genomic library using  
 CCA1 cDNA (see AAV65382) as probe. A claimed method for altering  
 plant response to daylength comprises transforming a plant with  
 either the CCA1 genomic DNA or cDNA, a hybridising sequence or a  
 nucleic acid encoding a protein containing amino acids 24-75 of the  
 608-amino acid CCA1 protein. Manipulation of plant circadian  
 rhythms (e.g. by overexpression of CCA1) can be used to delay  
 flowering, and thus increase yield from both forage crops, where  
 biomass will be produced for longer, and from seed crops such as  
 rape, where a longer time in vegetative state will lead to larger  
 plants and thus a higher seed set (claimed).

SQ Sequence 4344 BP; 1303 A; 808 C; 883 G; 1350 T; 0 other;

. Query Match

67.8%; Score 1527.6; DB 19; Length 4344;

	Best Local Similarity	87.9%;	Pred. No. 0;
	Matches 1803;	Conservative	0; Mismatches
		9;	Indels 240; Gaps
		3;	
QY	441	TTTCTCCAAAGGTAGAGAAAGAGGCTGAAGCTAAAGGTGTAGCTATGGTCAAGCGCTAGA	500
DB	2180	TCTCTCTCAGGTAGAGAAAGAGGCTGAAGCTAAAGGTGTAGCTATGGTCAAGCGCTAGA	2239
QY	501	CATAGCTATTCCTCTCCACCGCCCTAAGCGTAAACCAACAAATCCTTATCCTCGAAAGAC	560
DB	2240	CATAGCTATTCCTCTCCACCGCCCTAAGCGTAAACCAACAAATCCTTATCCTCGAAAGAC	2299
QY	561	GGGAAGTGGACGATCCTTATGTCAAAAACGGGTGTGAATCATCGAAAAAGTCCCTTGG	620
DB	2300	GGGAAGTGGACGATCCTTATGTCAAAAACGGGTGTGAATCATCGAAAAAGTCCCTTGG	2359
QY	621	ATCAGAAAAAGTGTCCGATCCCTG	643
DB	2360	ATCAGAAAAAGTGTCCGATCCTGAGTGATTTTCATGGTCATATGGCATCTTTTTCGAGT	2419
QY	644	-----	653
DB	2420	GTGTCACATGCTCCTCATGTTATTATACAGATTGTGTCTTCGTTTATAGATGGCCAA	2479
QY	654	TGAAGATCGAACAACAACTCAAGCCCTGAAGAGAAAACTCTGAGAGAACAACTGTTTCAGA	713
DB	2480	TGAAGATCGAACAACAACTCAAGCCCTGAAGAGAAAACTCTGAGAGAACAACTGTTTCAGA	2539
QY	714	TTGTTTCACTCATCAGTATCTCTCTGCTGCATCTCCATGAATAAAAGTTGTATAGAGAC	773
DB	2540	TTGTTTCACTCATCAGTATCTCTCTGCTGCATCTCCATGAATAAAAGTTGTATAGAGAC	2599
QY	774	ATCAACGCAAGCACTTTCCCGAGTTCTTCGCTTCACGGGAAG	817
DB	2600	ATCAACGCAAGCACTTTCCCGAGTTCTTCGCTTCACGGGAAGGATTAACAACTCT	2659
QY	818	-----	817
DB	2660	TTCAATTGCTATTTGAGGTTTTTAAGACGATTAGTACTTTTCATGAAACTAAAAACCGTGGG	2719
QY	818	-----AGGCAAGTTCAGAATAACAGGGTAAGAAAGGAGTCAAACTCAGATTTCGAATGCA	870
DB	2720	GAATTAACAGGGAGTTCAGATTACAGGGTAAGAAAGGAGTCAAACTCAGATTTCGAATGCA	2779
QY	871	AAATCTCTGAAAAACGGTAAATGAGCAAGGACCTCAGACTTATCCGATGCATATCCCTGTG	930
DB	2780	AAATCTCTGAAAAACGGTAAATGAGCAAGGACCTCAGACTTATCCGATGCATATCCCTGTG	2839
QY	931	CTAGTGCCATTGGGGAGCTCAATTAACAAGTTCTCTATCAGATCCTCTTCAGAGCCAGAT	990
DB	2840	CTAGTGCCATTGGGGAGCTCAATTAACAAGTTCTCTATCAGATCCTCTTCAGAGCCAGAT	2899
QY	991	AGTCATCCCCACACAGTTGAGGAGATTATCAGTCGTTTCCCTAATCATATAATGTCACAC	1050
DB	2900	AGTCATCCCCACACAGTTGAGGAGATTATCAGTCGTTTCCCTAATCATATAATGTCACAC	2959
QY	1051	CTTTTACAAAACCGGCTCTTTATATCGCGCAACTTTTCGCCCTCATCATTTTGGCCTCCC	1110
DB	2960	CTTTTACAAAACCGGCTCTTTATATCGCGCAACTTTTCGCCCTCATCATTTTGGCCTCCC	3019
QY	1111	GATTCTAGTGTGGCTCACCTGTTCCAGGGAACCTCACCTCCGAATCTGGCTGCCATGGCC	1170
DB	3020	GATTCTAGTGTGGCTCACCTGTTCCAGGGAACCTCACCTCCGAATCTGGCTGCCATGGCC	3079
QY	1171	GCAGCCACTGTTGCAGCTGCTAGTGCTTTGTTGGGTGCGCAATCGAATTATACCTTTATGT	1230
DB	3080	GCAGCCACTGTTGCAGCTGCTAGTGCTTTGTTGGGTGCGCAATCGAATTATACCTTTATGT	3139
QY	1231	GCTCCTCTTAGTTTCAGGTGGTTTTCACCTAGTCATCTCCATCTACTTACTTTGGACCATCATGT	1290
DB	3140	GCTCCTCTTAGTTTCAGGTGGTTTTCACCTAGTCATCTCCATCTACTTACTTTGGACCATCATGT	3199
QY	1291	GATGTAGAGTACAAAAAGCACTTTTACAACTATGTTCTGTGAGAGCCGAGAGCAA	1350

ID AAV09296 standard; DNA; 2526 BP.  
 XX AC AAV09296;  
 XX DT 07-JUL-1998 (first entry)  
 XX DE Nucleotide sequence of LHY gene.  
 XX KW Late elongated hypocotyl gene; LHY gene; flowering; day length;  
 XX KW transgenic plant; promoter; circadian oscillatory; ss.  
 XX OS Arabidopsis thaliana.  
 XX FH Key Location/Qualifiers  
 XX FT CDS 337..2275  
 XX FT /\*tag= a  
 XX FT /product= "LHY protein"  
 XX PN WO9749811-A1.  
 XX PD 31-DEC-1997.  
 XX PF 23-JUN-1997; 97WO-GB01676.  
 XX PR 21-JUN-1996; 96GB-0013132.  
 XX PA (INNE-) INNES CENT INNOVATIONS LTD JOHN.  
 XX PI Coupland GW, Schaffer RJ;  
 XX WP I: 1998-077174/07.  
 XX DR P-PSDB; AAW42084.  
 XX PT New isolated late elongated hypocotyl gene - used to obtain plants  
 XX PT with altered flowering characteristics, and for expression of  
 XX PT sequences under circadian rhythm control  
 XX PS Claim 4; Fig 1; 90pp; English.  
 XX CC This nucleotide sequence is of the late elongated hypocotyl (LHY)  
 XX CC gene, which is one of the genes that controls the timing of flowering  
 XX CC in relation to the length of day. The LHY type genes and derivatives  
 XX CC can be used for producing transgenic plants in which a physical  
 XX CC characteristic, such as a flowering characteristic which may include  
 XX CC timing of flowering, is affected. The LHY promoters can be used to  
 XX CC regulate expression of a sequence of interest in a circadian  
 XX CC oscillatory manner.  
 XX SQ Sequence 2526 BP; 767 A; 523 C; 528 G; 708 T; 0 other;  
 Query Match 9.6%; Score 217.2; DB 19; Length 2526;  
 Best Local Similarity 49.9%; Pred. No. 6.3e-46;  
 Matches 986; Conservative 0; Mismatches 823; Indels 165; Gaps 11;  
 QY 235 GTGATGGAGACAAATTCGCTCGAGAAGATCTGGTTATTAAAGACTCGGAAGCCATATACG 294  
 DB 335 GTTATGGATCTAATACATCTCGAGAAGAAATTATTAGCTAAGGCAAGAAAGCCATATACA 394  
 QY 295 ATACAAAGCAGCGTGAAGGTGGACTGAGGAAGAACATAATAGATTTCATTGAAGCTTTG 354  
 DB 395 ATACAAAGCAGCGAGCGATGGACTGAGGATGACCATGACAGGTTTCTAGAAGCCTTG 454  
 QY 355 AGGCTTTATGGTAGCATGGCAGAAAGATTGAAGAACATGTAGCAACAAAACTGCTGTC 414  
 DB 455 AGGCTTTATGGAAGAGCTTGGCAACGAATTGAAGAACATATTGGGACAAAGACTGCTGTT 514  
 QY 415 CAGATAAGAGTCACGCTCAGAAAATTTTCTCCAAGGTAGAGAAAGGCTGAAGCTAAA 474  
 DB 515 CAGATCAGAAGTCATGCAAAAGTCTTTCACAAAGTTGGAGAAAGAGGCTGAAGTTAAA 574  
 QY 475 GGTGTAGCTATGGGTCAAGCGCTAGACATAGCTATTTCCTCCACGGCTTAAGCGTAAA 534  
 DB 575 GGCATCCCTGTTTGGCAAGCTTTGGACATAGAAATTCGGCTCTCTGCTCTTAACGAA 634

QY 535 CCAAAACAATCCTTATCTCTCGAAGACGGAAGTGAACGATCCTTATGTCAAAAACGGGT 594  
 DB 635 CCAATACTCCTTATCTCGAAGAACTGGGAACAACCGGTACATCTTCTCTCAAGATACA 694  
 QY 595 GTGAATGATGGAAGAGTCCCTTGGATCAGAAAAAGTGTGGATCTCTGATGTGGCAAT 654  
 DB 695 TCAGCAAAAGATGCAAAACTTGTTCATCGGCTCTTCTTACAGTTGAAATCAGGCGTTC 754  
 QY 655 GAAGATCGACAACAATCAAAAGCCTGAAGAGAAAAC-----TCTGCAGGAA 699  
 DB 755 TTGGATTGGAANAATGCGGTTCTCTGAGAAAACATCAACTCGAANAAGAAAATCAAGAT 814  
 QY 700 GAACTGTTTCAGATTGTTTCACTCATCATGATATCTCTCTGCTGCATCTCCATGAATAAAA 759  
 DB 815 GAGAAATTGCTCGGTGTTTCTACTGTGAACAAGTATCCCTTACCAAGAAACAGGTAAGT 874  
 QY 760 AGTTGTATAGACATCAAAACGACACTTT-----CCGGAGTTCTTGGCTTC 809  
 DB 875 GCGCATTTGAAACAAGTAAGACCTCAACTGTGGACAACGCGGTTCAAGATGTTCCCAAG 934  
 QY 810 ACGGGAAGAGGGAAGTCAGAATAACAGGGTA-----AGAAAGGAGTCAAC 855  
 DB 935 AAGAACAAGACAAAGATGGTAACGATGGTACTACTGTGCACAGCATGCAAAACTACCT 994  
 QY 856 TCAGATTGGAATGCAAAATCTCTGGAACCGGTAAATGAGCAAGGACTCTCAGACTTATCC- 914  
 DB 995 TGGCATTTCCACGAGATATTGTGAACGGGAATATAGCAAAATGCCCTCAAAATCATCCC 1054  
 QY 915 -----G 915  
 DB 1055 TCAGGTATGGTATCTCAAGACTTTCATGTTTTCATCTCTATGAGAGAAGAACTACGGGCAC 1114  
 QY 916 ATGCATATCCCTGTGCTAGTGCCATTGGGGAGCTCAATAACAAGTTCTCTATCACAATCCT 975  
 DB 1115 GCAATCTTCAAGCTACAACAGCATCTGCTACTACTACAGCTTCTCATCAAGCGTTTCCA 1174  
 QY 976 CTTTCAGAGCCAGATAGTATCATCCCAACACAGTTGTCAGGAGATTTATCAGCTGTTCTTAAT 1035  
 DB 1175 GCTTGTCTATTCAGAGATGATTACCGTTCTGTTTCTCCAGATATCATCTTCTCCAAT 1234  
 QY 1036 CATATAATGTCAAACCTTTTACAACACCGGCTCTTTATACCTGCGCAACTTTTGGCTCA 1095  
 DB 1235 CTTATTATGTCAACTCTCTCAGAAATCTCGAGCTCATGCTGCAGCTACATTGCGTCT 1294  
 QY 1096 TCATTTTGGCCTCCCG-----ATTCTAGTGGTGGCTCACCTGTTTCAGGGAAC 1143  
 DB 1295 TCGGTCTGGCCTTATGCGAGTGTGGGAATCTGGTGATTTCATCAACCCCAATGAGCTCT 1354  
 QY 1144 TCACCTCCGAATCTGGCTGCCATGGCCGAGCCACTGTTTGCAGCTGCTAGTGTCTGGTGG 1203  
 DB 1355 TCTCTCTCAAGTATAACTGCCATTGCCGCTGCTACAGTAGCTGCTGCAACTGCTTGGTGG 1414  
 QY 1204 GCTGCAATGGATTAATTAACCTTTATGCTCTCTTCTTGTAGTTCAGGTGGTTTCACTAGTCAT 1263  
 DB 1415 GCTTCTCATGAGCTTCTTCTCTGTATGCGCTCCAGCTCCAATAACATGTGTCTCATCTCA 1474  
 QY 1264 CTTCCATCTACTTTTGGACCATCATGTGATGTAGATACACAAAACGACGACTTTACAA 1323  
 DB 1475 ACTGTTGAGTTTCAACTCCAGCAATGACTGAAATGGATACCGTTGAAAATATCTCAACCG 1534  
 QY 1324 CATGTTTCTGTGACAGCGGAGCAAGAACTCCGAGGCACTCAAGGCTCGACTTTCA 1383  
 DB 1535 TTTGAGAAACAAAACACAGCTCTGCAAGATCAAACTTGGCTTGAATCTCCAGGTTCA 1594  
 QY 1384 CTGAGCTCAGAGGATGTTGAAAAT-----AAGAGTAAACCAAGTTTGTGATGAGCAG 1434  
 DB 1595 TCATCTGATGATTAGATGAGACTGGAGTAACCAAGCTAAATGCCGACTCAAAAACCAAT 1654  
 QY 1435 CTTCTGCAACACCTGAGAGTGATGCAA-----AGGTTTCAGATGGAGCAGA 1482  
 DB 1655 GATGATAAAATTGAGGAGGTTGTTGTTACTGCGCTGTGTGATGACTCAAAACACTGCCAG 1714







635 CCCAATCTCTTATCTCGGAAACCTGGGAAACCGGTACATCTTCTCTCAAGTATCA 694  
Qy  
595 GTGAATGATGGAAGAAGTCCCTTGGATCAGAAAAAGTGTGCAATCTCTGAGATGSCCAAT 654  
Db  
695 TCAGCAAAAGATGCAAAACTTGTTCATCGGCTCTTCTTCAAGTGAATCAGCGGTC 754  
Qy  
655 GAAGATCGAACAACATCAAGCCCTGAAGAGAAAC-----TCTCAGGAA 699  
Db  
755 TTGATTTGGAAAAATGCGCTTCTCTGAGAAAAACATCAACTGGAAGAAAAATCAAGAT 814  
Qy  
700 GACAACTGTTTCAGATTTTTCACATCATCAGTATCTCTCTGCTGCATCTCTCATGAATAAA 759  
Db  
815 GAGAAATGCTCGGCTGTTCTACTGTGAACAAGTATCCCTTACCAACGAACAGGTAAGT 874  
Qy  
760 AGTTGTATAGACATCAAGCGAAGCACTTT-----CCGCGAGTTCTTGCCTTC 809  
Db  
875 GGCACATTTGAAAACAAGTAAGACCTCAACTGTGACCAACGCGTTCAAGATGTTCCCAAG 934  
Qy  
810 ACGGAAGAGGGAAGTCAGATAACAGGTA-----AGNAGGAGTCAAC 855  
Db  
935 AAGAACAAAGCAAGATGGTAACGATGGTACTACTGTGCACACATGCAAAACTACCC 994  
Qy  
856 TCAGATTTGAATGCAAAATCTCTGAAAAACGGTAATGAGCAAGACCTCAGACTTATCC- 914  
Db  
995 TGGCATTTCCACGCGAGATATTGTGAACGGGAATATAGCAAAATGCCCTCAAATCATCCC 1054  
Qy  
915 -----G 915  
1055 TCAGGTATGGTATCTCAAGACTTCATGTTTCATCTCTATGAGAGAAACCTCACGGCAC 1114  
Qy  
916 ATGCATATCCTGTGCTAGTGCCATTCGGGAGCTCAATACAGTCTCTATCATCATCCT 975  
Db  
1115 GCAAACTCTCAAGCTACAACAGCATCTGCTACTACAGCTTCTCATCAAGCGTTTCCA 1174  
Qy  
976 CTTTCAGAGCCAGATAGTCTATCCCCACACAGTTGCGAGGATATCAGTCTGTTCCCTAAT 1035  
Db  
1175 GCTTGTCTTACAGGATGATTACCGTTTCGTTCTCCAGATATCATCTACTTCTCCAA 1234  
Qy  
1036 CATATAATGTCAACCTTTTACAAACACCGGCTCTTTATCTGCGGCAACTTTGCGCTCA 1095  
Db  
1235 CTTATTATGTCAACTCTCTACAGAACTCTGCGAGCTATGCTGCGAGTACATCTGCTGCT 1294  
Qy  
1096 TCATTTTGGCTCCCG-----ATTCTAGTGGTCCCTCACCTGTTCCAGGAAC 1143  
Db  
1295 TCGGTCTGGCTTATGCGAGTGTGGGAATCTTGTGTGATTCATCAACCCCAATGAGCTCT 1354  
Qy  
1144 TCACCTCCGAATCTGGTGCATCGGCGCAGCCACTGTGCGAGCTGTAGTCTGTGTGG 1203  
Db  
1355 TCTCTCCAAAGTATAACTGCCATTCGCGCTGTACAGTAGCTGCTGCAACTGCTTGTGG 1414  
Qy  
1204 GCTGCCAATGGATATTACCTTTATGTGCTCTCTTATGTTTCAAGTGTGTTTCACTAGTCAT 1263  
Db  
1415 GCTTCTCATGGACTTCTTCTGTATGCGCTCCAGCTCCAATAACATGTGTTCCATTCTCA 1474  
Qy  
1264 CCTCCATCTACTTTTGGACCATCATGTGATGTAGGTACACAAAGCAACACTTTACAA 1323  
Db  
1475 ACTGTTGCACTTCAACTCCAGCAATGACTGAATGGATACCGTTGAAAATATCTCAACCG 1534  
Qy  
1324 CATGGTTCTGTGAGAGCCGAGAGCAAGAACACTCCGAGGCATCAAAAGGCTCGACTTTCA 1383  
Db  
1535 TTTGAGAAACAAACACAGCTCTGCAAGATCAAACTTGGCTTCGAAATCTCCAGTTCA 1594  
Qy  
1384 CTGGACTCAGAGATGTTGAAAT-----AAGATTAACAGTTTCTCATGAGCAG 1434  
Db  
1595 TCATCTGTGATGATTCAGATGAGCTGGAGTAACCAAGCTAAATGCCACTCAAAACCAAT 1654  
Qy  
1435 CCTTCTGCAACACTCAGAGTGTATGCAA-----AGGTTTCAGATGAGCAGGA 1482  
Db  
1655 GATGATAAAATTCAGAGAGGTTGTTGTTATGCGCGCTGTGTCATGACTCAAAACACTGCCCG 1714  
Qy  
1483 GACAGAAAAACAGTTGACCGGCTCTCTGTTGGCTCAAAACACTCCGTCGAGTAGTGATGAT 1542  
Db  
1715 AAGAAAAATCTTGTGACCGCTCATCTGTGTGGCTCAAAATACACTTCAGGGAGTGACGCA 1774

## RESULT 9

AAD05761

ID AAD05761 standard; cDNA; 2526 BP.

AC AAD05761;

XX 31-JUL-2001 (first entry)

XX Arabidopsis thaliana transcription factor homologue G680 cDNA.

XX Transcription factor; trait modification; seed characteristic;

XX structural characteristic; developmental characteristic; gene therapy;

XX agricultural biotechnology; ss.

XX Arabidopsis thaliana.

FH Key Location/Qualifiers

CDS 338..2275

FT /\*tag= a

FT /product= "Transcription factor homologue G680"

FN WO200135727-A1.

XX 25-MAY-2001.

XX 14-NOV-2000; 2000MO-US31457.

XX 17-NOV-1999; 99US-0166228.

PR 17-APR-2000; 2000US-0197899.

PR 22-AUG-2000; 2000US-0227439.

XX (MEND-) MENDEL BIOTECHNOLOGY INC.

PA (REUB/) REUBER L.

PA (CREE/) CREELMAN R.

PA (PILG/) PILGRIM M.







CC to a wild-type or reference plant, or the plant exhibits an altered  
CC phenotype as compared to a wild-type or reference plant, or the plant  
CC exhibits ectopic expression or altered expression of one or more genes  
CC associated with a plant trait as compared to a wild plant. Also included  
CC are a transgenic plant comprising the polynucleotides, a computer  
CC readable medium having stored sequence information, and identifying a  
CC homologue sequence from a database comprising a plurality of known plant  
CC sequences comprising inputting sequence information selected from one of  
CC 464 fully defined sequences given in the specification. The isolated or  
CC recombinant polynucleotide is used for producing a plant having a  
CC modified trait, the method comprising selecting a polynucleotide that  
CC encodes a polypeptide or an antisense nucleic acid, inserting the  
CC polynucleotide or antisense nucleic acid into an expression vector,  
CC introducing the vector into a plant or a cell of a plant to overexpress  
CC the polypeptide or antisense nucleic acid, thereby producing a modified  
CC plant, and selecting for a modified trait (e.g. increased  
CC production of agriculturally useful proteins or metabolic chemicals,  
CC pest tolerance, environmental stress response (e.g. drought), microbial  
CC disease resistance, herbicide resistance, seed and fruit yield, growth  
CC rate, leaf and flower senescence and many other traits listed in the  
CC specification). The present sequence is one of the 232 polynucleotides  
CC encoding an A. thaliana transcription factor.  
XX  
SQ Sequence 2526 BP; 767 A; 523 C; 528 G; 708 T; 0 other;

Query Match 9.6%; Score 217.2; DB 24; Length 2526;  
Best Local Similarity 49.9%; Pred. No. 6.3e-45;  
Matches 986; Conservative 0; Mismatches 823; Indels 165; Gaps 11;

CC	856	TCAGATTGTAATGCAAAATCTCTGGAACCGTAATGAGCAAGGACCTCAGACTTTATCC-	914
D	856		
D	995	TGGCATTTCCACGCGAGATATTGTGACCGGAATATAGCAAAATGCGCTCAAAATCATCC	1054
Q	915	-----	G 915
D	1055	TCAGGTATGGTATCTCAAGACTTCATGTTTTCATCTATGAGAGAAGAAACTCACGGCAC	1114
Q	916	ATGCATATCCCTGTGCTAGTGCCATGGGAGCTCAATAACAAGTTCTCTATCATCATCT	975
D	1115	GCAATCTTCAAGCTACACAGCATCTGTACTACTACAGCTTCTCATCAAGCGTTTCA	1174
Q	976	CTTTCAGAGCCAGATCTATCCCAACACAGTTTCAGGAGATTATCAGTCGTTTCTTAAT	1035
D	1175	GCTTGTCATTCACAGGATGATTACCGTTTCTCCAGATATCATCTACTTCTCCAAAT	1234
Q	1036	CATATATGTCACACCTTTTACAAACACCGCTCTTTATATCTGCGCAACTTTGCGCTCA	1095
D	1235	CTTATATGTCACCTCTCTACAGAACTCTGACATCTATGTCAGCTTACATTCGCTGCT	1294
Q	1096	TCATTTTGGCTCCCG-----ATTCTAGTGGTGGCTCACCTGTTCCAGGGAAAC	1143
D	1295	TCGCTCTGGCTTATGCGAGTGTGGGAATTTCTGGTATTCATCAACCCCAATGAGCTCT	1354
Q	1144	TCACCTCCGAATCTGGCTGCCATGGCGCAGCCACTGTTGCGAGCTGTAGTCTTGTGGTG	1203
D	1355	TCTCTCCAAATGATAAATGCAATGCGCTGTCTACAGTAGCTGTGCAACTGCTTGTGG	1414
Q	1204	GCTGCCAATGGATTATTAACCTTTATGTCCTCTTTAGTTCAGGTGTTTCACTAGTCAAT	1263
D	1415	GCTTCTCATGGACTTCTTCTGTATGCGCTCCAGCTCCAATAACATGTGTTCCATTTCTCA	1474
Q	1264	CCTCCATCTACTTTTGGACCATCATGTGATCTAGAGTACACAAAGCAAGCACTTACAA	1323
D	1475	ACTGTTGCGAGTTCCAACTCCAGCAATGACTGAAATGGATACCGTTGAAAATACTCAACCG	1534
Q	1324	CATGGTTCTCTGCGAGCCGAGCAAGAACACTCCGAGGACTCAAAAGGCTCGATCTTCA	1383
D	1535	TTTGAGAAACAAACACAGCTCTGCAAGATCAAACTTGGCTTCAAAATCTCCAGCTTCA	1594
Q	1384	CTGACTCAGAGGATTTGAAAT-----AAGAGTAAACAGTTTGTCTAGTAGCAG	1434
D	1595	TCATCTGATGATTCAGATGAGACTGGAGTAAACCAAGCTAAATGCGACTCAAAACCAAT	1654
Q	1435	CCTTCTGCAACACCTGAGAGTGATGCAA-----AGGTTTCAGATGGAGCAGGA	1482
D	1655	GATGATAAAATGAGGAGGTTGTTTACTGCGCTGTGATGACTCAAACTGCGCCAG	1714
Q	1483	GACAGAAACCAAGTTGACCGGTCTCTGTTGGCTCAAAACACTCCGTGAGTAGTGATGAT	1542
D	1715	AAGAAAAATCTTGTGGACCGCTCATCGTGTGGCTCAAAATACACCTTCAGGAGTGACGCA	1774
Q	1543	GTTGAGCGGATGATCAGAAAGCAAGAGATGGCACCAATGTTGAGGTGAAAGAAACG	1602
D	1775	GAAACTGATGATTAAGATAAAATGGAGAAAGATAAGAGGATGTGAAGGAGACAGATGAG	1834
Q	1603	AAT-----GAAGACACTATAAACCTCAAACTTCAGAGTCCATGACCGCGCAGTAGA	1656
D	1835	AATCAGCGAGATGTTTATGATTAATTAACCGTAAGATTAAATGAGAGACAAACAGCAGC	1894
Q	1657	ATCAGCTTCCAATATAACCGATCCATGGAAGTCTGTCTGACAGGGGTGCAATTTGCGCTTC	1716
D	1895	AACAACTTCACTACTGATTCGTGGAAGAAAGTCTCCGAGAGGGTCTGATATAGCGTTT	1954
Q	1717	CAAGCTCTCTTCTCAGAGAGGATTGTCGCCCAAGTTTATATATCGAAGAGAACACAGA	1776
D	1955	CAGGCTCTCTTTCAGAGAGAAAGATTGCTTCAAAAGCTTTTTCGCTCTCTCAAGTGGCAGAG	2014
Q	1777	GAGGAGAGAACAAACAAACAGAACAAAGATATCCCATGGCACTTGATCTTAATCTTCA	1836
D	2015	AATGTGATAGAAACAAAGTGACAGT-----CAATGCCATTTGGCTCTCAATTTCAAA	2068
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Db 2069 AGCCAGGATCTTGTGCTGCAGACCAAGA-----AGGAGTAGTAATGATC 2113  
QY 1897 GGATTAGATGCTTCAAAGCTAATGAGTAGAGAGAGAACAGAGTCTTAAACCATACAAAGA 1956  
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QY 1957 TGTTCATGGAAGCAAGAAAGTAGAATCCCTCAACAACAATCCCTATCATTCATGTGGAA 2016  
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RESULT 12

ABZ13311  
ID ABZ13311 standard; DNA; 1938 BP.  
XX AC ABZ13311;  
XX DT 21-JAN-2003 (first entry)  
XX DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1116.  
XX KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.  
XX OS Arabidopsis thaliana.  
XX PN WO200216655-A2.  
XX PD 28-FEB-2002.  
XX PF 24-AUG-2001; 2001WO-US26685.  
XX PR 24-AUG-2000; 2000US-227866P.  
XX PR 26-JAN-2001; 2001US-264647P.  
XX PR 22-JUN-2001; 2001US-300111P.  
XX PA (SCRI ) SCRIPPS RES INST.  
XX PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX PI Harper JF, Kreps J, Wang X, Zhu T;  
XX WPI; 2002-304127/34.  
PT Identifying a stress condition to which a plant cell has been exposed  
PT and producing plants with increased tolerance to these abiotic stresses  
PS Claim 144; SEQ ID NO 1116; 577pp + Sequence Listing; English.

XX The invention relates to identifying a stress condition to which a plant  
XX cell has been exposed, comprising:  
XX (a) contacting nucleic acid representative of expressed polynucleotides  
XX in the plant cell with an array or probes representative of the plant  
XX cell genome; and  
XX (b) detecting a profile of expressed polynucleotides in the plant cell  
XX characteristic of a stress response. The method is useful in the  
XX production of transgenic plants, cells and seeds and in producing plants  
XX with increased tolerance to abiotic stress. The present sequence is that  
XX of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used  
XX in methods of the invention.  
XX Note: The sequence data for this patent is not represented in the printed  
XX specification but is based on sequence information supplied to Derwent by  
XX the European Patent Office.

XX Sequence 1938 BP; 632 A; 417 C; 418 G; 471 T; 0 other;

Query Match 9.4%; Score 213; DB 24; Length 1938;  
Best Local Similarity 49.9%; Pred. No. 6.8e-45;  
Matches 980; Conservative 0; Mismatches 820; Indels 165; Gaps 11;

QY 238 ATGAGAGCAAAATTCGTCTGGAGAGAGATCTGCTTATTAGACTCGGAAGCCATATACGATA 297  
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QY 358 CTTTATGTTAGAGCATGGCAGAGATTTGAAGAAACATGTTAGCAACAAAACTGCTGTCAG 417  
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QY 703 AACTGTTGAGATGTTGTTCACTCATCAGTATCTCTGCTGTCATCTCTCATGAATAAAAGT 762  
Db 481 AATTGCTCGGGTGTCTTCTACTGTGAACAAAGTATCCCTTACCAACGAAACAGGTAAGTGGC 540  
QY 763 TGTATAGAGACATCAACGCAAGCACTTTTC-----GCGAGTTCTTGCTTCCAG 812  
Db 541 GACATTTGAAACAAGTAAGACCTCACTGTGTGCAACGCGGTTCAAGATGTTTCCCAAGAG 600  
QY 813 GGAAGAGGGAAGTCAAGATTAACAGGTTA-----AGAAAGAGGTCAAACTCA 858  
Db 601 AACAAAGACAAAGATGTTAAGTGTACTACTGTGACAGCATGTCAAAATACCTCTGG 660  
QY 859 GATTGTAATGCAAAATCTCTGGAACCGTAAATGAGCAAGACCTCAGACTTATCC---- 914  
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Db 1021 CCTCCAAAGTATAACTGCCCATTTGGCGCTGCTACAGTAGCTGTGCAACTGCTTGGTGGCT 1080







KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
XX metabolic pathway; promoter; termination sequence; ss.  
OS Arabidopsis thaliana.

PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
XX  
PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
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PR 30-APR-1999; 99US-0132048.  
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GenCore version 5.1.1.6  
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Listing first 45 summaries

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29: gb\_gsl2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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C 2	485.4	21.5	487	9	AI992931
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C 4	422.2	18.7	439	9	AV792310

5	395.8	17.6	515	9	AA394931	AA394931	26812	Lam
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C 12	356.2	15.8	423	9	AV807633	AV807633	AV807633	
C 13	315.6	14.0	403	9	AV799191	AV799191	AV799191	
14	292.4	13.0	334	9	AV831875	AV831875	AV831875	
15	292.4	13.0	580	9	AV827752	AV827752	AV827752	
C 16	240.8	10.7	396	9	AV818056	AV818056	AV818056	
17	215.6	9.6	805	14	CB293827	CB293827	UCRCS01	
18	206.8	9.2	771	13	BU868664	BU868664	M118F07	
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C 21	195.6	8.7	202	9	AV800550	AV800550	AV800550	
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#### ALIGNMENTS

RESULT 1  
AQ958316/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AQ958316 740 bp DNA linear GSS 28-JAN-2000  
LERAW81TF LERA Arabidopsis thaliana genomic clone LERAW81, genomic  
survey sequence.  
AQ958316 GI:6786017  
AQ958316.1  
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Arabidopsis thaliana  
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
1 (bases 1 to 740)  
Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T.,  
Felblym, T., Liang, F., Creasy, T. and Fraser, C.M.  
Genomic survey sequencing of Landsberg erecta ecotype of  
Arabidopsis thaliana and identification of sequence-based  
polymorphisms  
Unpublished  
Contact: Xiaoying Lin  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: at@tigr.org  
For additional information, see <http://www.tigr.org/tdb/at/at.html>

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Class: Shotgun.
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/notes="Organ: Leaf; Vector: pHOS1; Total genomic DNA was
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CDNA clone 701495069, mRNA sequence.  
AI992931  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source  
BASE COUNT 160 a 105 c 115 g 107 t  
ORIGIN  
Query Match 21.5%; Score 485.4; DB 9; Length 487;  
Best Local Similarity 99.8%; Pred. No. 3.7e-73;  
Matches 486; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 466 GAAGCTAAAGGTGTAGCTATGGGTCAAGCGCTAGACATAGCTATTCCTCTCCACGCGCT 525  
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Db 61 AAGCGTAAACCAACAACTCTTATCTCGAAAGACGGGAAGTGGACGATCTTATGTCA 120  
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Db 181 ATGGCCAAATGAAGTCAACAACTCAAGCCCTGAAGAGAAAACCTCTGCAAGGAACAAC 240  
QY 706 TGTTCAGATGTTTCTACTCATCAGTATCTCTGCTGCATCTTCCATGAATAAAGTTGT 765  
Db 241 TGTTCAGATGTTTCTACTCATCAGTATCTCTGCTGCATCTTCCATGAATAAAGTTGT 300  
QY 766 ATAGACATCAAAACCAAGCACTTTCGCGAGTCTTTCGCTTTCACGGGAAGGGAAGT 825  
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QY 826 CAGAATAACAGGGTAGAAGAGGAGTCAAACTCAGATTTGAATGAAAATCTCTGGAAAAC 885  
Db 361 CAGAATAACAGGGTAGAAGAGGAGTCAAACTCAGATTTGAATGAAAATCTCTGGAAAAC 420  
QY 886 GGTAATGAGCAAGGACCTCAGACTTTATCCGATGCATATCCCTGTGTAGTGGCAATGGGG 945

AI992931  
LOCUS  
DEFINITION 487 bp mRNA linear EST 08-SEP-1999  
CDNA clone 701495069, mRNA sequence.  
AI992931  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source  
BASE COUNT 160 a 105 c 115 g 107 t  
ORIGIN  
Query Match 21.5%; Score 485.4; DB 9; Length 487;  
Best Local Similarity 99.8%; Pred. No. 3.7e-73;  
Matches 486; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 466 GAAGCTAAAGGTGTAGCTATGGGTCAAGCGCTAGACATAGCTATTCCTCTCCACGCGCT 525  
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QY 646 ATGGCCAAATGAAGTCAACAACTCAAGCCCTGAAGAGAAAACCTCTGCAAGGAACAAC 705  
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QY 766 ATAGACATCAAAACCAAGCACTTTCGCGAGTCTTTCGCTTTCACGGGAAGGGAAGT 825  
Db 301 ATAGACATCAAAACCAAGCACTTTCGCGAGTCTTTCGCTTTCACGGGAAGGGAAGT 360  
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Db 361 CAGAATAACAGGGTAGAAGAGGAGTCAAACTCAGATTTGAATGAAAATCTCTGGAAAAC 420  
QY 886 GGTAATGAGCAAGGACCTCAGACTTTATCCGATGCATATCCCTGTGTAGTGGCAATGGGG 945







3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-4359  
Fax: 81-298-36-9060  
Email: mseki@rtc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLIC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pluescript vector. Please visit our web site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further details.

#### FEATURES

Location/Qualifiers

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/organism="Arabidopsis thaliana"

/mol\_type="mRNA"

/db\_xref="taxon:3702"

/clone="RAFL09-81-L16"

/dev\_stage="plants at various developmental stages from germination to mature seeds"

/lab\_host="DH10B"

/clone\_lib="RAFL9"

/note="Site 1: BamHI; Site 2: SalI; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24 hr) treatments"

BASE COUNT 126 a 70 c 74 g 123 t

#### ORIGIN

Query Match 17.4%; Score 393; DB 9; Length 393;

Best Local Similarity 100.0%; Pred. No. 2.6e-57;

Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1836 AGCTCAGTTTAAACACCGATGATCAAGAGGAGAGAAACACAGGATTTCTTGGAAAT 1895

DB 393 AGCTCAGTTTAAACACCGATGATCAAGAGGAGAGAAACACAGGATTTCTTGGAAAT 334

QY 1896 CGGATTAGATGCTTCAAGCTAATGATGAGGAGAGAAACAGGTTTAAACCATACAAAG 1955

DB 333 CGGATTAGATGCTTCAAGCTAATGATGAGGAGAGAAACAGGTTTAAACCATACAAAG 274

QY 1956 ATGTTTCCATGGAAGCCAAAGAAAGTAGAATCTCTCAACAACAATCTATCATCTGGA 2015

DB 273 ATGTTTCCATGGAAGCCAAAGAAAGTAGAATCTCTCAACAACAATCTATCATCTGGA 214

QY 2016 ACAGAAAGATCCAAACCGATCGGTTGAAACTCAAGCTTCCACATGAGACTCTATTTT 2075

DB 213 ACAGAAAGATCCAAACCGATCGGTTGAAACTCAAGCTTCCACATGAGACTCTATTTT 154

QY 2076 CATCTGATCTGTTGTTGACTCTGTTTTTAAGTTTTCAAGACCACCTGCTACATTTCTT 2135

DB 153 CATCTGATCTGTTGTTGACTCTGTTTTTAAGTTTTCAAGACCACCTGCTACATTTCTT 94

QY 2136 TTCTTTTGAAGCCCTTGATTTGTTTCTTGTCCATAGTCTTCTGTAAACATTTGACTC 2195

DB 93 TTCTTTTGAAGCCCTTGATTTGTTTCTTGTCCATAGTCTTCTGTAAACATTTGACTC 34

QY 2196 TGTATTATCAACAATCAATAACTGTTTAAATC 2228

DB 33 TGTATTATCAACAATCAATAACTGTTTAAATC 1

#### RESULT 7

AV801368/c

LOCUS AV801368 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-27-N02 3',  
DEFINITION mRNA sequence.

ACCESSION AV801368

VERSION AV801368.1 GI:19835353

KEYWORDS EST.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

#### REFERENCE

##### AUTHORS

1 (bases 1 to 396)

Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,  
Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,  
Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.  
and Shinozaki, K.

##### TITLE

##### JOURNAL

##### COMMENT

Large scale analysis of Arabidopsis full-length cDNA (2002b)

Unpublished

Contact: Motoaki Seki

Plant Functional Genomics Research Group

RIKEN Genomic Sciences Center

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: 81-298-36-4359

Fax: 81-298-36-9060

Email: mseki@rtc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLIC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pluescript vector. Please visit our web site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further details.

#### FEATURES

Location/Qualifiers

1..396

/organism="Arabidopsis thaliana"

/mol\_type="mRNA"

/db\_xref="taxon:3702"

/clone="RAFL09-27-N02"

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/lab\_host="DH10B"

/clone\_lib="RAFL9"

/note="Site 1: BamHI; Site 2: SalI; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24 hr) treatments"

BASE COUNT 133 a 68 c 74 g 121 t

#### ORIGIN

Query Match

Best Local Similarity 17.0%; Score 384; DB 9; Length 396;

Matches 395; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1844 TAACACCGATTGATGATCAAGAGGAGAGAAACACAGGATTTCTTGGAAATCGGATTAG 1903

DB 396 TAACACCGATTGATGATCAAGAGGAGAGAAACACAGGATTTCTTGGAAATCGGATTAG 337

QY 1904 ATGCTTCAAGCTTAATGAGTAGAGGAGAACAGGTTTAAACCATACAAAGATGTTCCA 1963

DB 336 ATGCTTCAAGCTTAATGAGTAGAGGAGAACAGGTTTAAACCATACAAAGATGTTCCA 277

QY 1964 TGAAGCCAAAGAAAGTAGAATCTCAACAACAATCTATCATTCATGTGGAACAGAAAG 2023

DB 276 TGAAGCCAAAGAAAGTAGAATCTCAACAACAATCTATCATTCATGTGGAACAGAAAG 217

QY 2024 ATCCCAACCGATGCGGTTGGAAACTCAAGCTTCCACATGAGACTCTATTTTCATCTGAT 2083

DB 216 ATCCCAACCGATGCGGTTGGAAACTCAAGCTTCCACATGAGACTCTATTTTCATCTGAT 157

QY 2084 CTGTTGTTGTACTCTGTTTTTAAGTTTTTCAAGACCACCTGCTACATTTCTTTTCTTTT 2143

DB 156 CTGTTGTTGTACTCTGTTTTTAAGTTTTTCAAGACCACCTGCTACATTTCTTTTCTTTT 98

QY 2144 GAGGCCCTTTGATTTGTTTCTTGTCCATAGTCTTCTGTAAACATTTGACTCTGTATTAT 2203

DB 97 GAGGCCCTTTGATTTGTTTCTTGTCCATAGTCTTCTGTAAACATTTGACTCTGTATTAT 38

QY 2204 TCAACAATCATAAACTGTTTAAATCTTTTTTTTTC 2239

DB 37 TCAACAATCATAAACTGTTTAAATCTTTTTTTTTC 2

#### RESULT 8

AV823536

LOCUS

AV823536 628 bp mRNA linear EST 01-APR-2002

DEFINITION AV823536 RAFL5 Arabidopsis thaliana cDNA clone RAFL05-20-N17 5', mRNA sequence.

ACCESSION AV823536

VERSION AV823536.1 GI:19865596

KEYWORDS EST.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE 1 (bases 1 to 628)

AUTHORS Seki M., Narusaka M., Ishida J., Kamiya A., Satou M., Nakajima M., Oono Y., Sakurai T., Carninci P., Kawai J., Itoh M., Ishii Y., Arakawa T., Shibata K., Shingawa A., Muramatsu M., Hayashizaki Y., and Shinozaki K.

TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)

JOURNAL Unpublished

COMMENT Contact: Motoaki Seki  
Plant Functional Genomics Research Group  
RIKEN Genomic Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-4359  
Fax: 81-298-36-9060  
Email: mseki@rtc.riken.go.jp  
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a modified pBluescript vector as a SstI/XhoI insert. Please visit our web site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further details.

FEATURES	source	Location/Qualifiers
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		/dev_stage="rosette plants"
		/lab_host="SOLR"
		/clone_lib="RAFL5"
		/note="Site 1: SstI; Site 2: XhoI"
194 a	94 c	dehydration-treated(1,2,5,10,24
BASE COUNT	194 a	127 g 210 t

Query Match	16.8%;	Score 378.4;	DB 9;	Length 628;
Best Local Similarity	99.5%;	Pred. No. 7.2e-55;		
Matches 390;	Conservative 0;	Mismatches 1;	Indels 1;	Gaps 1;
QY	65	ACTCTCTCTCTCTCTCTCTCTCGATTCCTACTGTTTCTTATCCAAAGAAATCTCGAAT	124	
Db	2	ACTCTCTCTCTCTCTCTCTCTCGATTCCTACTGTTTCTTATCCAAAGAAATCTCGAAT	61	
QY	125	TAAAAATGGAATCTTTTATTCGAATCCAAAG-CTGATTTTGGTTTCTTTCATTCGAATCATCTCT	183	
Db	62	TAAAAATGGAATCTTTTATTCGAATCCAAAGCTGATTTTGGTTTCTTTCATTCGAATCATCTCT	121	
QY	184	CTAAAGTGGAAATTTTGTAAAGAGAAGATCTCGAAGTCTGTAGAGGAGCTTTAGTGATGGAG	243	
Db	122	CTAAAGTGGAAATTTTGTAAAGAGAAGATCTCGAAGTCTGTAGAGGAGCTTTAGTGATGGAG	181	
QY	244	ACAAATTCGTCTGGAGAAGATCTGGTTATTAAAGACTCGGAAGCCATATACGATAACAAAG	303	
Db	182	ACAAATTCGTCTGGAGAAGATCTGGTTATTAAAGACTCGGAAGCCATATACGATAACAAAG	241	
QY	304	CAACCTGAAAGGTGGACTCTGAGGAAGACATAATAGATTTCATTGAAGCTTTGAGGCTTTAT	363	
Db	242	CAACCTGAAAGGTGGACTCTGAGGAAGACATAATAGATTTCATTGAAGCTTTGAGGCTTTAT	301	
QY	364	GGTAGAGCAATGCGAGAAGATTGAAGAAACATGTTAGCAACAAAACACTGCTCTCCAGATAAGA	423	
Db	302	GGTAGAGCATGGCAGAAGATTGAAGAAACATGTTAGCAACAAAACACTGCTCTCCAGATAAGA	361	
QY	424	AGTCACGCTCAGAAATTTTCTCCAAAGGTAGA	455	

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362 AGTCACGCTCAGAAATTTTCTCCAAGGTAAA 393

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T41938
LOCUS
DEFINITION
5201 Lambda-PRL2 Arabidopsis thaliana cDNA clone 109K917, mRNA
sequence.
ACCESSION
T41938
VERSION
T41938
KEYWORDS
EST.
SOURCE
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 480)
AUTHORS
Newman,T., deBruin,F.J., Green,P., Keegstra,K., Kende,H., McIntosh
,L., Ohriogger,J., Raikhel,N., Somerville,S., Thomasow,M., Retzel
,B. and Somerville,C.
TITLE
Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
JOURNAL
Plant Physiol. 106, 1241-1255 (1994)
MEDLINE
95148729
PUBMED
7846151
COMMENT
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
Lansing, Mi
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@bm.cl.msu.edu
Seg primer: T7.

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FEATURES	SOURCE
1. <b>High Accuracy:</b> The model achieves a high accuracy rate, consistently performing well across various datasets and tasks.	1. <b>High Accuracy:</b> The model achieves a high accuracy rate, consistently performing well across various datasets and tasks.
2. <b>Scalability:</b> The model is designed to handle large-scale data and complex tasks, making it suitable for enterprise-level applications.	2. <b>Scalability:</b> The model is designed to handle large-scale data and complex tasks, making it suitable for enterprise-level applications.
3. <b>Interpretability:</b> The model provides clear and understandable explanations for its predictions, enhancing transparency and trust.	3. <b>Interpretability:</b> The model provides clear and understandable explanations for its predictions, enhancing transparency and trust.
4. <b>Robustness:</b> The model is highly robust to noise and outliers, ensuring reliable performance in real-world scenarios.	4. <b>Robustness:</b> The model is highly robust to noise and outliers, ensuring reliable performance in real-world scenarios.
5. <b>Efficiency:</b> The model is optimized for fast processing and low resource consumption, making it ideal for resource-constrained environments.	5. <b>Efficiency:</b> The model is optimized for fast processing and low resource consumption, making it ideal for resource-constrained environments.

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/contig="vector.Lambda Zip-Lox; S
Lambda PRU2 is a cDNA library de
quantities of 4 pools of mRNA.
day germinated etiolated seedling
grown roots; 3) staged plants ha
cycle, half on 16 hr light, 8 ho
same plants as 3 but aerial tiss
siliques. The vector is BRL's l
inserts were directionally clone
oligo dt primed cDNA. "
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BASE COUNT  
ORIGIN

Query Match	16.4%	Score 369.2;	DB 14;	Length 480;
Best Local Similarity	94.0%;	Pred. No. 2.9e-53;		
Matches 451; Conservative	0;	Mismatches 22;	Indels 7;	Gaps 7;
QY	466	GAAGCTAAAGGTTAGCTATGGGTCAAGCGCTAGACATAGTCTATTCCTCTCCACGGCCT	525	
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Db	121	AAACCGGGTGTGAATGATGGAAGAGTCCCTTGGTTCAGAAAAAGTGTCCGATCCTTGAG	180	
QY	646	ATGGCCAATCAAGATCGACAACAATCAAAAGCCTGGAAGAGAAAACTCTGCAGGAAGACAAC	705	

Db 181 ATGGCCATGAAGATCGACAACATCAAGACCTGGAAGAGAAACCTTCGAGGAAGACAAC 240

Qy 706 TGTTCAGATTGTTTCACTCATCATGATCTCTCTGCTGCATCTCTCCATCAATGAATAAAGATTCT 765

Db 241 TWTTCAGATTGTTTCACTCATCATGATCTCTCTGCTGCATCTCCATCAATGAATAAAGATTCT 300

Qy 766 ATAGAGACATCAAA-CGGAGACATTTCCGCGAG-TTCTTGCTTCCACGGAA-GAGGGA 822

Db 301 ATAGNGCATCAAAACCGAAGACATTTCCGCGAGTTCTTGNCTTCAACGGGAGGAGGA 360

Qy 823 ACTCAGATAACAGGGTAAG-AAAGGAGTCAAACTCAGATTTCGAATGC-AAATCTCTCG 880

Db 361 ACTCAGNATAACAGGGTGAAGAAAGGAGTCAAACTCAGGTTTGAATTCAAAATCTCTG 420

Qy 881 AAAACGGTAA-TGACGAAGGACCTCAGACTTATCC-GATGCAATATCCCTGTGCTAGTGCC 938

Db 421 AAAACGGTAATTNGCAAGNCTCAGACTTTTNCGGTTGAATATCCCTGTGCGAGTGCC 480

RESULT 10  
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LOCUS LERAW81TR LERA Arabidopsis thaliana genomic clone LERAW81, genomic survey sequence.

ACCESSION AQ958317  
VERSION AQ958317.1 GI:6786018  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana

REFERENCE  
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; euroids II; Brassicales; Brassicaceae; Arabidopsis.  
Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T., Fiedlmyer, T., Liang, F., Creasy, T. and Fraser, C.M.  
TITLE Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based polymorphisms  
JOURNAL Unpublished  
COMMENT Contact: Xiaoying Lin  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: at@tigr.org  
For additional information, see <http://www.tigr.org/tdb/at/at.html>  
Seq primer: TR  
Class: shotgun.

## FEATURES

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/clone="LERAW81"  
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/note="Organ: Leaf; Vector: PHOS1; Total genomic DNA was sheared to 0.9-1 kbp before ligation."

BASE COUNT 90 a 108 c 84 g 111 t

ORIGIN

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Best Local Similarity 98.4%; Pred. No. 9.3e-53;  
Matches 370; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 857 CAGATTGTAATCAAAATCTCGAAACGGTAATGAGCAAGACCTCAGACTTATCCGA 916

Db 13 CAGATTGTAATCAAAATCTCGAAACGGTAATGAGCAAGACCTCAGACTTATCCGA 72

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Db 133 CTTCAGAGCCAGATAGTCATCCCAACACAGTTGACAGGAGATTATCAGTCGTTTCCTTAATC 192

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Db 193 ATATAATGTCAACCCCTTTTACAAACACCGGCTCTTTATCTAGTGGGACACTTTCGCCTCAT 252

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Db 253 CATTTTGGGCTCCCGATTTAGTGGTGGCTCACCTGTTCAGGGAACCTCACCTCCGAATC 312

Qy 1157 TGGTCCCATGCGCGAGCCACTGTTCGAGCTCTAGTGTGTTGGGCTGCCAATGGAT 1216

Db 313 TGGTCCCATGCGCGAGCCACTGTTCGAGCTCTAGTGTGTTGGGCTGCCAATGGAT 372

Qy 1217 TATTACCTTTATGTGC 1232

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## RESULT 11

AV784525/c  
LOCUS AV784525 RAFL5 Arabidopsis thaliana cDNA clone RAFL05-20-N17 3', mRNA sequence.

ACCESSION AV784525  
VERSION AV784525.1 GI:19803315  
KEYWORDS EST.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana

REFERENCE  
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; euroids II; Brassicales; Brassicaceae; Arabidopsis.  
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.

TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)  
JOURNAL Unpublished  
COMMENT Contact: Motoaki Seki  
Plant Functional Genomics Research Group  
RIKEN Genomic Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-4359  
Fax: 81-298-36-9060  
Email: msekic@tcr.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a modified pBluescript vector as a SstI/XhoI insert. Please visit our web site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further details.

## FEATURES

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/note="Site 1: SstI; Site 2: XhoI; subjected to dehydration-treated(1,2,5,10,24 hr)"

BASE COUNT 128 a 59 c 69 g 104 t

ORIGIN

Query Match 16.0%; Score 360; DB 9; Length 360;  
Best Local Similarity 100.0%; Pred. No. 1.2e-51;  
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QY 2023 GATCCAAACGATGCGGTTGAACTCAAGCTCCACATGAGAGCTATTTTCATCTGA 2082  
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QY 2083 TCTGTTGTTGTTACTCTGTTTAAAGTTTCAAGACCACTGCTACATTTCTTTTCTTT 2142  
Db 164 TCTGTTGTTGTTACTCTG- TTTTAAAGTTTCAAGACCACTGTTTAAATTTTCTTTT 106

QY 2143 TGAGGCTTTT---GTATTGTTTCTTGTCCATAGTCTTCTCTGT---AACATTTGACTC 2195  
Db 105 TGAGGCTTTTGTATTGTTTCTTGTCCATAGTCTTCTCTGT---AACATTTGACTC 46

QY 2196 TGTATTATTCACAAATCAAACTGTTTAACTTTTAACTTTTCTTTTCTTTTCTTTTCC 2239  
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RESULT 14  
AV831875  
LOCUS AV831875 RAFL9 Arabidopsis thaliana cdna clone RAFL09-96-L16 5',  
DEFINITION mRNA sequence.  
ACCESSION AV831875.1 GI:19873935.  
VERSION AV831875  
KEYWORDS EST.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
; eurosids II; Brassicales; Brassicaceae; Arabidopsi  
1 (bases 1 to 334)  
REFERENCE  
AUTHORS Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,  
Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,  
Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.  
and Shinozaki,K.  
Large scale analysis of Arabidopsis full-length cdna (2002b)  
Unpublished  
Contact: Motoaki Seki  
Plant Functional Genomics Research Group  
RIKEN Genomic Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-4359  
Fax: 81-298-36-9060

Email: mseki@rtc.riken.go.jp  
An Arabidopsis full-length cdna library was constructed essentially as reported previously (Seki et al., 1998).cdna cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index\_e.html) for further details.

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113 a 47 C 78 G 93 t 3 others

BASE COUNT  
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Query Match 13.0%; Score 292.4; DB 9; Length 334;  
Best Local Similarity 99.7%; Pred. No. 4.6e-40;  
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QY 402 AAAAAGCTGCTCCAGATAAGAGTCACGCTCAGAAATTTTCTCCAGGTAGA 455  
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LOCUS AV827752 RAFL9 Arabidopsis thaliana cdna clone RAFL09-19-A10 5',  
DEFINITION mRNA sequence.  
ACCESSION AV827752  
VERSION AV827752.1 GI:19869812  
KEYWORDS EST.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
; eurosids II; Brassicales; Brassicaceae; Arabidopsi  
1 (bases 1 to 580)  
REFERENCE  
AUTHORS Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,  
Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,  
Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.  
and Shinozaki,K.  
Large scale analysis of Arabidopsis full-length cdna (2002b)  
Unpublished  
Contact: Motoaki Seki  
Plant Functional Genomics Research Group  
RIKEN Genomic Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: 81-298-36-4359  
Fax: 81-298-36-9060  
Email: msek@rtc.riken.go.jp  
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pluescript vector. Please visit our web site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further details.

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            /lab\_host="DH10B"  
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ORIGIN

Query Match      13.0%; Score 292.4; DB 9; Length 580;  
Best Local Similarity 99.7%; Pred. No. 3.9e-40;  
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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QY      282    GAAGCCATATACGATTAACAAGCAACGTGAAGGTGGACTGAGGAAGACATAATAGATT 341  
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QY      342    CATTGAAGCTTTGAGGCTTTATGGTAGCATGGCAGAGATTGAAGACATGTAGCAAC 401  
DB      181    CATTGAAGCTTTGAGGCTTTATGGTAGCATGGCAGAGATTGAAGACATGTAGCAAC 240  
QY      402    AAAAAGCTGTCTCCAGATAAGAGTCACGCTCAGAAATTTTCTCCAAGGTAGA 455  
DB      241    AAAAAGCTGTCTCCAGATAAGAGTCACGCTCAGAAATTTTCTCCAAGGTAAA 294

Search completed: November 24, 2003, 13:01:56  
Job time : 4444.81 secs





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## RESULT 2

US-08-843-572E-1

; Sequence 1, Application US/08843572E  
; Patent No. 6388172  
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; APPLICANT: TOBIN, ELAINE  
; APPLICANT: WANG, ZHI-YONG  
; APPLICANT: SUN, LIN  
; TITLE OF INVENTION: PHYTOCHROME REGULATED  
; TITLE OF INVENTION: TRANSCRIPTION FACTOR FOR CONTROL OF HIGHER PLANT  
; TITLE OF INVENTION: DEVELOPMENT  
; FILE REFERENCE: P601-D-36315.60100  
; CURRENT APPLICATION NUMBER: US/08/843,572E  
; CURRENT FILING DATE: 1997-04-18  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Microsoft Word 7.0 (DOS text file)  
; SEQ ID NO 1:

; LENGTH: 4344  
; TYPE: DNA  
; ORGANISM: Arabadopsis/thalia  
US-08-843-572E-1

Query Match 67.8%; Score 1527.6; DB 4; Length 4344;  
Best Local Similarity 87.9%; Pred. No. 0;  
Matches 1803; Conservative 0; Mismatches 9; Indels 240; Gaps 3;  
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RESULT 3
US-09-202-712-1
; Sequence 1, Application US/09202712
; Patent No. 6265637
; GENERAL INFORMATION:
; APPLICANT: Coupland, George M
; APPLICANT: Schaffer, Robert J
; TITLE OF INVENTION: Genetic control of flowering
; FILE REFERENCE: 620-55
; CURRENT APPLICATION NUMBER: US/09/202,712
; CURRENT FILING DATE: 1999-01-11
; EARLIER APPLICATION NUMBER: PCT/GB97/01676
; EARLIER FILING DATE: 1997-06-23
; EARLIER APPLICATION NUMBER: GB 9613132.1
; EARLIER FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2526
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (338)..(2275)
US-09-202-712-1

Query Match      9.6%; Score 217.2; DB 3; Length 2526;
Best Local Similarity 49.9%; Pred. No. 2.6e-49;
Matches 986; Conservative 0; Mismatches 823; Indels 165; Gaps 11;

Qy      235 GTGATGAGACAAATTCGTCTGGAGAGATCGTGTATTAGACTCGGAAGCCATATACG 294
Db      235 GTTATGATACATACTCTGGAGAGAAATTTATTAGCTAAGGCAAGAAAGCCATATACA 394

Qy      295 ATAAACAAAGCAACGTGAAAGGTGGAAGTGAAGAGAAACATAATAGATTCAATGAAAGCTTTG 354
Db      295 ATAAACAAAGCAGCAGAGCGATGACTGAGATGAGCATGAGAGTTCTTAGAAGCCTTG 454

Qy      355 AGGCTTTATGATAGCATGCGCAGAGATTTGAAGAACATGATAGCAACAAACAACTGCTGC 414
Db      455 AGGCTTTATGGAAGAGCTTGGCAACGAAATTTGAAGAACATATTTGGGCAAAAGACTGCTGT 514

Qy      415 CAGATAAAGACTCAGCTCAGAAATTTTCTCCAGGTAGAGAGAGGCTGAAGCTAAA 474
Db      515 CAGATCAGAGTATGCACAAAGTTCTTCAAAAGTTGGAGAAAGAGGCTGAAAGTTAAA 574

Qy      475 GGTGTAGCTATGGTCAAGCGCTAGACATAGCTATTCTCTCCACCGGCTTAAGCGTAAA 534
Db      575 GGCATCCTGTTGCCAAGCTTTGGACATAGAAATTCGCGCTCTCGTCTTAACGAAAA 634

Qy      535 CCAACAACTCTTATCTCGAAAGACGGGAAGTGGAAAGTCCCTTATGTCAAAAACGGGT 594
Db      635 CCCAATACTCTTATCTCGAAAAACCTGGGAACACACGATACATCTCTCTCAAGTATCA 694

Qy      595 GTGAATGATGAAAAGAGTCCCTTTGGATCAGAAAAGTGTCCGATCTCGATCGCCAT 654
Db      695 TCAGCAAAAGATGCAAAACTTGTTTCATCGGCCCTCTCTTCCACAGTTGAAATCAGCGGTC 754

Qy      655 GAAGATCGACAAACATCAAGCGCTGAAGAGAAAAAC-----TCTCAGGAA 699
Db      755 TTGGATTGGAAAAAATGCCGTTCTCTGAGAAAAACATCAACTGGAAGAAATCAAGAT 814

Qy      700 GACAACTGTTTCAGATTGTTTCACTCATCATGATATCTCTGCTGTCATCTCCATGAATAAA 759
Db      815 GAGAAATTCGTCGGGTGTTTCTACTGTGAACAAGTATCCCTTTACCAACGAAACAGGTAAGT 874

Qy      760 AGTTGTATAGACATCAACCGCAAGCACTTT-----CCGCGAGTTCTTGCCTTC 809
Db      875 GCGACATTGAAACAGTAAAGACCTCACTGTGTGACAAACGCGGTTCAAGATGTTCCCAAG 934

Qy      810 ACGGAGAGGGAAGTCAGAAATACAGGGTA-----AGAAAGGAGTCAAAC 855
Db      935 AAGAACAAAGACAAAGATGGTAACGATGGTACTACTGTGCACAGCATCAAAACATACCT 994

Qy      856 TCAGATTGTAATGCAAAATCTCTGGAACCGGTAAATGAGCAAGGACCTCAGACTTTATCC- 914
Db      995 TGGCATTTCCACGCGAGATATTGTGAACGGGAATATAGCAAAATGCCCTCAAAATCATCCC 1054

Qy      915 -----G 915

Db      1055 TCAGGTATGGTATCTCAAGACTTTCATGTTTCATCTATGAGAGAGAAACTCACGGCAC 1114

Qy      916 ATGCATATCCCTGTGCTAGTCCCATTTGGGAGCTCAATAACAAAGTTCTCTATCATCATCT 975
Db      1115 GCAAAATCTTCAAGCTTACAAAGCATCTGCTACTACTACAGCTTCTCATCAAGCGTTTCCA 1174

Qy      976 CTTTCAGAGCCAGATAGTATCTCCCAACACACAGTTGCGAGAGATTATCAGTCGTTTCTTAAT 1035
Db      1175 GCTTGTCAATTCACAGGATGATTACGGTTCGTTTCTCCAGATATCATCTACTTCTCCAT 1234

Qy      1036 CATATAATGTCAACCCCTTTTACAACACCGGCTCTTTATATCTGCGCAACTTTCGCCTCA 1095
Db      1235 CTTATTATGTCAACTCTCTACAGAAATCTGCGAGCTCATGCTGCGAGCTACATTCGCTGCT 1294

Qy      1096 TCATTTTGGCTCCCG-----ATTCTAGTGGTGGCTCACCTGTTCCAGGGGAA 1143
Db      1295 TCGGTCTGGCCCTTATGCGAGTGTGCGGAATTTCTGGTGATTTCATCAACCCCAATGAGTCT 1354

Qy      1144 TCACCTCCGAATCTGGCTGCGCAGCGACCACTGTTGCAGCTGCTAGTGTCTGTTGG 1203
Db      1355 TCTCCTCCAAGTATAACTGCCATTTGCCGCTGCTACAGTAGCTGTGCAACTGCTGTTGG 1414

Qy      1204 GCTGCCAATGGAATTAATACCTTTATGCTCCTCTTATGTTTCTAGTTTCTAGTGTGTTT 1263
Db      1415 GCTTCTCATGAGACTTCTTCTGTATGGCTCCAGCTCCAATAACATGTTGTTCCATCTCA 1474

Qy      1264 CTTCCATCTACTTTTGGACCATCATGATGTAGGTACACAAAGCAAGCACTTTACNA 1323
Db      1475 ACTGTTGAGTTTCCAACTCCAGCAATGACTGAAATGGATACCGTTGAAATACTCAACCG 1534

Qy      1324 CATGGTTCTGTGACAGCCGAGACAAACACCTCCGAGGCGATCAAAAGGCTCGATCTTCA 1383
Db      1535 TTTGAGAAACAAACACACAGCTCTCGAAGATCAAACTTGGCTTCGAATCTCCAGCTTCA 1594

Qy      1384 CTGACTCAGAGGATGTTGAAAT-----AAGAGTAAACAGGTTTGTGATGAGCAG 1434
Db      1595 TCATCTGATGATTTCAGATGAGACTGGAGTAAACCAAGCTAAATGCCGACTCAAAAAACCAAT 1654

Qy      1435 CTTTCTGCAACACCTGAGAGTGATGCAA-----AGGTTTCAGATGGAGCAGGA 1482
Db      1555 GATGATAAAATTTGAGGAGGTTGTTGTTACTGCGCGCTGTGCATGACTCAAAACATGCCCCAG 1714

Qy      1483 GACAGAAAAAAGTTGACCGGCTCCTGTTGGCTCAAAACACTCCGTCGAGTAGTGATGAT 1542
Db      1715 AAGAAAAATCTTGTGGACCGCTCATCTGTGGCTCAATAACACTTCAAGGAGTGACCGCA 1774

Qy      1543 GTTGAGGGGATGATCAGAAAGCAAGAGATGGCAACCAATGTGTAGGTGAAAGAAACG 1602
Db      1775 GAAACTGATGATTTAGATAAAATGGAGAAAGATAAAGAGGATGTGAAGGAGACAGATGAG 1834

Qy      1603 AAT-----GAAGACACTTAATAACCTCAAACTTCAGAGTCCAATGACCGCGCAGTAGA 1656
Db      1835 AATCAGCCAGATGTTATTGAGTTAAATAACCGTAAGATTAAATGAGAGACAAACACAGC 1894

Qy      1657 ATCAGCTCCAATATAACCGGCTCCTGTTGGAAGTCTGTCTGACGAGGGTCAATTTGCGCTTC 1716
Db      1895 AACAAACAATGCAACTACTGATTCTGTGGAAGGAAGTCTCCGAGAGGGTCTGTATAGCGTTT 1954

Qy      1717 CAAGCTCTCTTCTCAGAGAGGATTATCCCGAAAGTTTATCATATCAGAGAGAAACACAGA 1776
Db      1955 CAGGCTCTCTTTGCAAGAGAAAGATTGCTCAAAAGCTTTTTCGCTCTCTCAAGTGGCAGAG 2014
```

















Qy	121	GAATTTAAAAATGGAAATCTTTTATCGAATCCAAGCTGATTTTGTTTCTTTTCATTGTAATCATC	180
Db	121	GAATTTAAAAATGGAAATCTTTTATCGAATCCAAGCTGATTTTGTTTCTTTTCATTGTAATCATC	180
Qy	181	TCTCTAAAGTGGAAATTTTGTAAAGAGAAGATCTGAAGTTGTGTAGAGGAGCTTGTAGTGATG	240
Db	181	TCTCTAAAGTGGAAATTTTGTAAAGAGAAGATCTGAAGTTGTGTAGAGGAGCTTGTAGTGATG	240
Qy	241	GAGACAAATTCGTCTGGAGAGAATCTGTTTATTAGACTCGGAAGCCATATACGATAACA	300
Db	241	GAGACAAATTCGTCTGGAGAGAATCTGTTTATTAGACTCGGAAGCCATATACGATAACA	300
Qy	301	AAGCAACTGAAAGTGGACTCGAGAAGAAATATAATAGATTCAATTGAAGCTTTTGAGGCTT	360
Db	301	AAGCAACTGAAAGTGGACTCGAGAAGAAATATAATAGATTCAATTGAAGCTTTTGAGGCTT	360
Qy	361	TATGTTAGAGCATGGCAGAAGAATTGAAGAAATGTAGCAACAAAAACTGCTGTCAGATA	420
Db	361	TATGTTAGAGCATGGCAGAAGAATTGAAGAAATGTAGCAACAAAAACTGCTGTCAGATA	420
Qy	421	AGAAGTCAAGCTCAGAAAATTTTTTCTCAAGGTAGAGAAAGGCTGAAGCTTAAAGGTGA	480
Db	421	AGAAGTCAAGCTCAGAAAATTTTTTCTCAAGGTAGAGAAAGGCTGAAGCTTAAAGGTGA	480
Qy	481	GCTATGGTCAAGCGCTAGACATAGCTATTCTCTCCACGGCCTTAAGCGTAAACCAAC	540
Db	481	GCTATGGTCAAGCGCTAGACATAGCTATTCTCTCCACGGCCTTAAGCGTAAACCAAC	540
Qy	541	AATCTTTATCTCGAAAAGCGGAAGTGGAAACGATCTTATGTCAAAAAACGGGTGTGAAT	600
Db	541	AATCTTTATCTCGAAAAGCGGAAGTGGAAACGATCTTATGTCAAAAAACGGGTGTGAAT	600
Qy	601	GATGAAAAGAGTCCCTTGGATCAGAAAAAGTGTGCGATCTCGATAGATGGCCAAATGAAGT	660
Db	601	GATGAAAAGAGTCCCTTGGATCAGAAAAAGTGTGCGATCTCGATAGATGGCCAAATGAAGT	660
Qy	661	CGACAACAACTCAAAGCTGAGAGAAACACTCTCGCAGGAAGACAACTGTTTCAGATTGTTTC	720
Db	661	CGACAACAACTCAAAGCTGAGAGAAACACTCTCGCAGGAAGACAACTGTTTCAGATTGTTTC	720
Qy	721	ACTCATAGTATCTCTGTGTCATCTCTCCATGAATAAAAAGTTGTATAGACACATCAAAAC	780
Db	721	ACTCATAGTATCTCTGTGTCATCTCTCCATGAATAAAAAGTTGTATAGACACATCAAAAC	780
Qy	781	GCAAGCATTTCGGGAGTTCCTGGCTTCACGGGAAGGGAAGTCAAGATAACAGGGTA	840
Db	781	GCAAGCATTTCGGGAGTTCCTGGCTTCACGGGAAGGGAAGTCAAGATAACAGGGTA	840
Qy	841	AGAAAGGAGTCAAACTCAGATTTTGAATGCAAAATCTCTGGAACACGGTATGACACAGGA	900
Db	841	AGAAAGGAGTCAAACTCAGATTTTGAATGCAAAATCTCTGGAACACGGTATGACACAGGA	900
Qy	901	CCTCAGACTTATCCGATGCATATCCCTGTGCTAGTGCATTTGGGGAGCTCAATAACAACT	960
Db	901	CCTCAGACTTATCCGATGCATATCCCTGTGCTAGTGCATTTGGGGAGCTCAATAACAACT	960
Qy	961	TCTCTATCAGATCTCTTCAGAGCCAGATAGTCATCCCAACAGTTGCGAGAGATTAT	1020
Db	961	TCTCTATCAGATCTCTTCAGAGCCAGATAGTCATCCCAACAGTTGCGAGAGATTAT	1020
Qy	1021	CAGTCGTTTTCTTAATCATATAATGTCAACCCCTTTTACAAACACCGGCTCTTTACTGTC	1080
Db	1021	CAGTCGTTTTCTTAATCATATAATGTCAACCCCTTTTACAAACACCGGCTCTTTACTGTC	1080
Qy	1081	GCAACTTTCGCCCTCATATTTTGGCCTCCCGATTTCTAGTGTGGCTCACCTGTTCCAGGG	1140
Db	1081	GCAACTTTCGCCCTCATATTTTGGCCTCCCGATTTCTAGTGTGGCTCACCTGTTCCAGGG	1140
Qy	1141	AACTCACCTCCGAATCTGGCTGCCATGGCCGACGCACTGTTGACGCTGCTAGTGTGG	1200
Db	1141	AACTCACCTCCGAATCTGGCTGCCATGGCCGACGCACTGTTGACGCTGCTAGTGTGG	1200

QY	1201	TGGGCTGCGCAATGGATTAATTAACCTTTATGTGCTCCTCTTAAGTTTCAGGTGTTTCACTAGT	1260
DB	1201	TGGGCTGCCAATGGATTAATTAACCTTTATGTGCTCCTCTTAAGTTTCAGGTGTTTCACTAGT	1260
QY	1261	CATCCTCCATCTACTCTTTTGGACCATCATGTGATGTGTAGAGTACACAAAGCAAGCACTTTA	1320
DB	1261	CATCCTCCATCTACTCTTTTGGACCATCATGTGATGTGTAGAGTACACAAAGCAAGCACTTTA	1320
QY	1321	CAACATGGTTCTGTGCGAGCCGAGACCAAGAACACCTCCGAGGCATCAAAAGGCTCGATCT	1380
DB	1321	CAACATGGTTCTGTGCGAGCCGAGACCAAGAACACCTCCGAGGCATCAAAAGGCTCGATCT	1380
QY	1381	TCACCTGGACTCAGAGGATGTTGAAATAAGAGGTAAACACAGTTTGTCTATGAGCAGCCTTCT	1440
DB	1381	TCACCTGGACTCAGAGGATGTTGAAATAAGAGGTAAACACAGTTTGTCTATGAGCAGCCTTCT	1440
QY	1441	GCAACACCTCAGAGTGTATGCAAAAGGGTTTCAGATGGAGCAGAGACAGAAACAAGTTGAC	1500
DB	1441	GCAACACCTCAGAGTGTATGCAAAAGGGTTTCAGATGGAGCAGAGACAGAAACAAGTTGAC	1500
QY	1501	CGGTTCCTCGTGTGGCTCAAAACATCCCGTCAAGTAGTATGATGTTGAGGCCGATGCATCA	1560
DB	1501	CGGTTCCTCGTGTGGCTCAAAACATCCCGTCAAGTAGTATGATGTTGAGGCCGATGCATCA	1560
QY	1561	GAAGGCGAAGAGGATGCGACCAATGGTGGAGCTCGAAAGAAACGAAATGAAGACACCTAATAA	1620
DB	1561	GAAGGCGAAGAGGATGCGACCAATGGTGGAGCTCGAAAGAAACGAAATGAAGACACCTAATAA	1620
QY	1621	CCTCAAACTTCAGAGTCCAAATGCAACCGCCAGTAGAATCAGCTCCAATATAACCGATCCA	1680
DB	1621	CCTCAAACTTCAGAGTCCAAATGCAACCGCCAGTAGAATCAGCTCCAATATAACCGATCCA	1680
QY	1681	TGGAAGTCTGTGCTGACGAGGGTCGAAATGCGCTTCCAGCTCTCTTCTCCAGAGAGGTA	1740
DB	1681	TGGAAGTCTGTGCTGACGAGGGTCGAAATGCGCTTCCAGCTCTCTTCTCCAGAGAGGTA	1740
QY	1741	TTGCCGCAAAAGTTTTACATATCGAGAAGAAACACAGAGAGGAAGAACAAACAACAAGAA	1800
DB	1741	TTGCCGCAAAAGTTTTACATATCGAGAAGAAACACAGAGAGGAAGAACAAACAACAAGAA	1800
QY	1801	CAAGATATCCAATGGCACTTGATCTTAACCTCACAGCTCAGTTAAACACAGTTGATGAT	1860
DB	1801	CAAGATATCCAATGGCACTTGATCTTAACCTCACAGCTCAGTTAAACACAGTTGATGAT	1860
QY	1861	CAAGAGAGGAAGAGAAACACAGGATTTCTTGGAAATCGGATACATGCTTCAAAAGCTTAATG	1920
DB	1861	CAAGAGAGGAAGAGAAACACAGGATTTCTTGGAAATCGGATACATGCTTCAAAAGCTTAATG	1920
QY	1921	AGTAGAGGAAGAACAGGTTTTAAACCATACAAAGATGTTCCAATGGAAGCCAAAGAAAGT	1980
DB	1921	AGTAGAGGAAGAACAGGTTTTAAACCATACAAAGATGTTCCAATGGAAGCCAAAGAAAGT	1980
QY	1981	AGAACTCTCAACACCAATCCTATCATCTGTGGAACAGAAAGATCCCAACCGATGCCG	2040
DB	1981	AGAACTCTCAACACCAATCCTATCATCTGTGGAACAGAAAGATCCCAACCGATGCCG	2040
QY	2041	TTGAAACTCAAGCTTCCATGAGACTCTATTTTTCATCTGATCTGTTGTTGATCTCTG	2100
DB	2041	TTGAAACTCAAGCTTCCATGAGACTCTATTTTTCATCTGATCTGTTGTTGATCTCTG	2100
QY	2101	TTTTTAAGTTTTTCAAGACCCTGCTACATTTTCTTTTCTTTTGTAGGCCCTTTGTATTGTT	2160
DB	2101	TTTTTAAGTTTTTCAAGACCCTGCTACATTTTCTTTTCTTTTGTAGGCCCTTTGTATTGTT	2160
QY	2161	TTCTTGTCCATAGTCTTCTCTGTAAACATTTTGACTCTGTATTATTTCACAAACATCATAACT	2220
DB	2161	TTCTTGTCCATAGTCTTCTCTGTAAACATTTTGACTCTGTATTATTTCACAAACATCATAACT	2220
QY	2221	GTTTAAATCTTTTTTTTTTTCAAAAAATAAAAAA 2254	
DB	2221	GTTTAAATCTTTTTTTTTTTCAAAAAATAAAAAA 2254	



QY 1681 TGAAGTCTGTGTCGACGAGGTCGAATTCGCTTCCAAAGCTCTCTTCTCCAGAGGTA 1740  
DB 1681 TGAAGTCTGTGTCGACGAGGTCGAATTCGCTTCCAAAGCTCTCTTCTCCAGAGGTA 1740  
QY 1741 TTCGCCAAAGTTTTACATATCGAGAAGAACACAGAGAGGAGAACACAAACAAAGAA 1800  
DB 1741 TTCGCCAAAGTTTTACATATCGAGAAGAACACAGAGAGGAGAACACAAACAAAGAA 1800  
QY 1801 CAAAGATATCAATGGCAGCTTGATCTTTAACTTTCACAGCTCAGTTAAACACAGTTGATGAT 1860  
DB 1801 CAAAGATATCAATGGCAGCTTGATCTTTAACTTTCACAGCTCAGTTAAACACAGTTGATGAT 1860  
QY 1861 CAAGAGAGAGAGAGAACACAGAGATTTCTTGGAAATCGGATTCGCTTCAAAGCTTAATG 1920  
DB 1861 CAAGAGAGAGAGAGAACACAGAGATTTCTTGGAAATCGGATTCGCTTCAAAGCTTAATG 1920  
QY 1921 AGTAGAGAGAGAGAGAGTTTTAAACCATACAAAGATGTTCCATGGAGCCAAAGAAAGT 1980  
DB 1921 AGTAGAGAGAGAGAGAGTTTTAAACCATACAAAGATGTTCCATGGAGCCAAAGAAAGT 1980  
QY 1981 AGAATCTTCAACAAATCTATCATTCATGTGGAAACAGAAAGATCCCAACCGATCGCG 2040  
DB 1981 AGAATCTTCAACAAATCTATCATTCATGTGGAAACAGAAAGATCCCAACCGATCGCG 2040  
QY 2041 TTGGAAGCTCAAGCTTCCACATGAGACTCTATTTTCACTCTGATCTGTGTGTGATCTCTG 2100  
DB 2041 TTGGAAGCTCAAGCTTCCACATGAGACTCTATTTTCACTCTGATCTGTGTGTGATCTCTG 2100  
QY 2101 TTTTAAAGTTTTCAAGACCACTGCTACATTTCTTTTCTTTTGGAGCCCTTCTGATTTGT 2160  
DB 2101 TTTTAAAGTTTTCAAGACCACTGCTACATTTCTTTTCTTTTGGAGCCCTTCTGATTTGT 2160  
QY 2161 TTCTTGTGCATAGTCTTCTGTAACATTTGACTCTGTATTTTCAACAAATCATAACT 2220  
DB 2161 TTCTTGTGCATAGTCTTCTGTAACATTTGACTCTGTATTTTCAACAAATCATAACT 2220  
QY 2221 GTTAAATCTTTTTTTTCCA 2240  
DB 2221 GTTAAATCTTTTTTTTCCA 2240

## RESULT 3

US-09-938-842A-1500  
; Sequence 1500, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; TITLE OF INVENTION: SAME, AND METHODS OF USE  
; FILE REFERENCE: SCRIPI300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 1500  
; LENGTH: 1827  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-1500

Query Match 81.1%; Score 1827; DB 10; Length 1827;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1827; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 238 ATGGAGACAAATTCGTCTGGAGAAGATCTGGTTATTATTAAGACTCGGAAGCCATATACGATA 297

DB 1 ATGGAGACAAATTCGTCTGGAGAAGATCTGGTTATTATTAAGACTCGGAAGCCATATACGATA 60  
QY 298 ACAAGCAACGCTGAAAGGTGGACTGAGGAAGAACATAATAGATTTCATTGAAGCTTTGAGG 357  
DB 61 ACAAGCAACGCTGAAAGGTGGACTGAGGAAGAACATTAATAGATTTCATTGAAGCTTTGAGG 120  
QY 358 CTTTATGTTAGACATCGGCAGAAAGATTGGAAGAACATGTAGCAACAAACAACTGCTGTCCAG 417  
DB 121 CTTTATGTTAGACATCGGCAGAAAGATTGGAAGAACATGTAGCAACAAACAACTGCTGTCCAG 180  
QY 418 ATAAGAGTCAACGCTCAGAAATTTTTCTCAAGGTAGAGAAAGAGGCTGAAGCTTAAAGGT 477  
DB 181 ATAAGAGTCAACGCTCAGAAATTTTTCTCAAGGTAGAGAAAGAGGCTGAAGCTTAAAGGT 240  
QY 478 GTAGCTATGGGTCAAGGGCTAGACATAGCTTATTCCTCTCAAGGGCTTAAGCTTAAACCA 537  
DB 241 GTAGCTATGGGTCAAGGGCTAGACATAGCTTATTCCTCTCAAGGGCTTAAGCTTAAACCA 300  
QY 538 AACAAATCCTTATCCTCGAAAGACGGGAAGTGGAAACGATCCTTATGTCAAAAACGGGTGTG 597  
DB 301 AACAAATCCTTATCCTCGAAAGACGGGAAGTGGAAACGATCCTTATGTCAAAAACGGGTGTG 360  
QY 598 AATGATGGAAAGAGTCCCTTGGATCAGAAAAAGTGTGCGATCCTGAGATGGCCAAATGAA 657  
DB 361 AATGATGGAAAGAGTCCCTTGGATCAGAAAAAGTGTGCGATCCTGAGATGGCCAAATGAA 420  
QY 658 GATCGAACAAATCAAGAGCTGAAGAAAGTCTGCGAGGAAGACAACTGTTTCAGATTGT 717  
DB 421 GATCGAACAAATCAAGAGCTGAAGAAAGTCTGCGAGGAAGAGGGAAGTCAAGATAACAGG 480  
QY 718 TTCACCTCATCAGTATCTCTCTGCTGCATCCTCCATGAATAAAGTTGTATAGAGACATCA 777  
DB 481 TTCACCTCATCAGTATCTCTCTGCTGCATCCTCCATGAATAAAGTTGTATAGAGACATCA 540  
QY 778 AACCGAAGCACTTTCCGCGAGTTCTTCCCTTACGGGAAGAGGGAAGTCAAGATAACAGG 837  
DB 541 AACCGAAGCACTTTCCGCGAGTTCTTCCCTTACGGGAAGAGGGAAGTCAAGATAACAGG 600  
QY 838 GTAAGAAAGAGTCAAACTCAGATTTTGAATGCAAAATCTCTGGAACAAAGTGAATGAGCAA 897  
DB 601 GTAAGAAAGAGTCAAACTCAGATTTTGAATGCAAAATCTCTGGAACAAAGTGAATGAGCAA 660  
QY 898 GGACCTCAGACTTATCCGATGCATATCCCTGCTAGTGCATTTGGGAGCTCAATAACA 957  
DB 661 GGACCTCAGACTTATCCGATGCATATCCCTGCTAGTGCATTTGGGAGCTCAATAACA 720  
QY 958 AGTTCTCTATCATCCTCTTCCAGAGCCAGATAGTCATCCCAACAGTTGCGAGGAGAT 1017  
DB 721 AGTTCTCTATCATCCTCTTCCAGAGCCAGATAGTCATCCCAACAGTTGCGAGGAGAT 780  
QY 1018 TATCAGTCTGTTTCCCTAATCATATAATGTCAACCTTTTACAAAACCGGCTCTTTTACT 1077  
DB 781 TATCAGTCTGTTTCCCTAATCATATAATGTCAACCTTTTACAAAACCGGCTCTTTTACT 840  
QY 1078 GCGCAACTTTGCGCTCATCATTTTGGCTTCCCGATTCTAGTGGTGGCTCACCTGTTCCA 1137  
DB 841 GCGCAACTTTGCGCTCATCATTTTGGCTTCCCGATTCTAGTGGTGGCTCACCTGTTCCA 900  
QY 1138 GGGAACTCACTCCGAATCTGGCTGCCATGGCGGAGCCACTGTTGAGCTGCTAGTGTCT 1197  
DB 901 GGGAACTCACTCCGAATCTGGCTGCCATGGCGGAGCCACTGTTGAGCTGCTAGTGTCT 960  
QY 1198 TGGTGGCTGCCAAATGGATTATTTACCTTTATGTGCTCTCTTAGTTTTCAGTGGTTCACT 1257  
DB 961 TGGTGGCTGCCAAATGGATTATTTACCTTTATGTGCTCTCTTAGTTTTCAGTGGTTCACT 1020  
QY 1258 AGTCATCTCTCCACTTACTTTTGGACCATCATGTGATGTAGAGTACACAAAGCAACACT 1317  
DB 1021 AGTCATCTCTCCACTTACTTTTGGACCATCATGTGATGTAGAGTACACAAAGCAACACT 1080  
QY 1318 TTACAACATGTTTGTGTCAGAGCCGAGAGCAAGAACACTCCGAGGATCAAGAGGCTCGA 1377

Db 1081 TTACAAACATGGTCTGTGTCAGAGCCGAGAGAGCAACACTCCGAGGCATCAAAAGGCTCGA 1140  
Qy 1378 TCCTCACTGCACTCAGAGGATGTTGAAAAATAAGAGTAAACCCAGTTCGTCTATGACAGCCT 1437  
Db 1141 TCCTCACTGCACTCAGAGGATGTTGAAAAATAAGAGTAAACCCAGTTCGTCTATGACAGCCT 1200  
Qy 1438 TCTGCAACACCTCAGAGTGTATGCAAGGGTTTCAGATGGAGCAGAGACAGAAAAACAAGTT 1497  
Db 1201 TCTGCAACACCTCAGAGTGTATGCAAGGGTTTCAGATGGAGCAGAGACAGAAAAACAAGTT 1260  
Qy 1498 GACCGTCTCGTGTGCTCAACACCTCCGTCGAGTAGTGTATGATGTTGAGCGGATGCA 1557  
Db 1261 GACCGTCTCGTGTGCTCAACACCTCCGTCGAGTAGTGTATGATGTTGAGCGGATGCA 1320  
Qy 1558 TCAGAAAGGCAAGAGTAGGCAACAATGGTGGAGTGAAGAAAAAGAAATGAAGACACTAAT 1617  
Db 1321 TCAGAAAGGCAAGAGTAGGCAACAATGGTGGAGTGAAGAAAAAGAAATGAAGACACTAAT 1380  
Qy 1618 AAACCTCAAACTTCAGAGTCAATGCAAGCGGCGAGTAGAATCAGCTCCAATATAACCGAT 1677  
Db 1381 AAACCTCAAACTTCAGAGTCAATGCAAGCGGCGAGTAGAATCAGCTCCAATATAACCGAT 1440  
Qy 1678 CCATGGAAGTCTGTCTGTCGAGGAGTCAATGCTCCCTTCAAGCTCTCTTCTCCAGAGAG 1737  
Db 1441 CCATGGAAGTCTGTCTGTCGAGGAGTCAATGCTCCCTTCAAGCTCTCTTCTCCAGAGAG 1500  
Qy 1738 GTATTGCGCAAAAGTTTTACATATCGAGAGAAACACAGAGAGGAGAAACAAACACAA 1797  
Db 1501 GTATTGCGCAAAAGTTTTACATATCGAGAGAAACACAGAGAGGAGAAACAAACACAA 1560  
Qy 1798 GAACAAAGATATCCAATGGCACTTGATCTTAACTTCACAGTCAAGTTAAACACAGTTGAT 1857  
Db 1561 GAACAAAGATATCCAATGGCACTTGATCTTAACTTCACAGTCAAGTTAAACACAGTTGAT 1620  
Qy 1858 GATCAAG 1917  
Db 1621 GATCAAG 1680  
Qy 1918 ATCAGTAG 1977  
Db 1681 ATCAGTAG 1740  
Qy 1978 AGTAGAATCTTCAACAACTATCTATCATTCATGTGGAAACAGAAAGATCCCAACCGATG 2037  
Db 1741 AGTAGAATCTTCAACAACTATCTATCATTCATGTGGAAACAGAAAGATCCCAACCGATG 1800  
Qy 2038 CGGTTGGAAGTCAAGCTTCCACATGA 2064  
Db 1801 CGGTTGGAAGTCAAGCTTCCACATGA 1827

## RESULT 4

US-10-084-553-1  
; Sequence 1, Application US/10084553  
; Publication No. US20030056247A1  
; GENERAL INFORMATION:  
; APPLICANT: Tobin, Elaine  
; APPLICANT: Wang, Zhi-Yong  
; APPLICANT: Sun, Lin  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Phytocrome Regulated Transcription Factor for Control  
; TITLE OF INVENTION: of Higher Plant Development  
; FILE REFERENCE: 023070-124200US  
; CURRENT APPLICATION NUMBER: US/10/084, 553  
; PRIOR FILING DATE: 2002-07-09  
; PRIOR APPLICATION NUMBER: US 08/843, 572  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 4344  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana

FEATURE:  
; OTHER INFORMATION: phytocrome-regulated transcriptional factor CCA1  
; OTHER INFORMATION: genomic clone

FEATURE:  
; NAME/KEY: exon  
; LOCATION: (1332)..(1370)  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (1371)..(1448)  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: (1449)..(1560)  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (1561)..(1648)  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: (1649)..(1710)  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (1711)..(2189)  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: (2190)..(2384)  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (2385)..(2471)  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: (2472)..(2645)  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (2646)..(2728)  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: (2729)..(3610)  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (3611)..(3680)  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: (3681)..(4043)  
; US-10-084-553-1

Query Match 67.8%; Score 1527.6; DB 14; Length 4344;  
Best Local Similarity 87.9%; Pred. No. 0;  
Matches 1803; Conservative 0; Mismatches 9; Indels 240; Gaps 3;

Qy 441 TTTCTCCAGGTAGAGAAAGAGGCTGAAGCTAAAGGTGTAGCTATGGTCAAGCGCTAGA 500  
Db 2180 TCTCTCTCAGGTAGAGAAAGAGGCTGAAGCTAAAGGTGTAGCTATGGTCAAGCGCTAGA 2239  
Qy 501 CATAGCTATTCTCTCCAGCGGCTAAGCGCTAAACCAAAACAATCTTATCTCGAAAGAC 560  
Db 2240 CATAGCTATTCTCTCCAGCGGCTAAGCGCTAAACCAAAACAATCTTATCTCGAAAGAC 2299  
Qy 561 GGGAAGTGGAAACCATCTTATGTCAAAACGGGTGGAATGATGGAAAAAGAGTCCCTTGG 620  
Db 2300 GGGAAGTGGAAACCATCTTATGTCAAAACGGGTGGAATGATGGAAAAAGAGTCCCTTGG 2359  
Qy 621 ATCAGAAAAAGTGTCCGATCCTG----- 643  
Db 2360 ATCAGAAAAAGTGTCCGATCCTGAGGTGATTTTCATGGTTCATATGGCATCTTTTTCAGT 2419  
Qy 644 -----AGATGGCCAA 653  
Db 2420 GTGTACATTGCTCTCTCATGTATTATAACAGATTGTGTCTCGTTTATAGATGGCCAA 2479  
Qy 654 TGAAGATCGACACAACTCAAGCGCTCAAGAGAAACTCTCGAGAGACAACTGTTTCAGA 713  
Db 2480 TGAAGATCGACACAACTCAAGCGCTCAAGAGAAACTCTCGAGAGACAACTGTTTCAGA 2539  
Qy 714 TTGTTTCACTCATCATCTCTCTCTGTCATCTCTCTGTCATCTCCATGAATAAAAAGTTGTATAGAGAC 773





; PRIOR FILING DATE: 2000-01-27  
; NUMBER OF SEQ ID NOS: 999  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 961  
; LENGTH: 479  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-770-961-961

Query Match 21.3%; Score 479; DB 11; Length 479;  
Best Local Similarity 100.0%; Pred. No. 6.6e-124; Indels 0; Gaps 0;  
Matches 479; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 502 ATAGCTATTCCTCCTCCACGGCTAAGCGTAACCAACCAATCCTTATCCTCGAAAGACG 561  
Db 1 ATAGCTATTCCTCCTCCACGGCTAAGCGTAACCAACCAATCCTTATCCTCGAAAGACG 60  
QY 562 GGAAGTGGACGATCCTTATGTCACCAACCGGTGTGAATGATGGAAGAGTCCCTTGGGA 621  
Db 61 GGAAGTGGACGATCCTTATGTCACCAACCGGTGTGAATGATGGAAGAGTCCCTTGGGA 120  
QY 622 TCAGAAAAAGTGTGCGATCCTGAGATGGCCCAATGAAGATCGACAAATCAAGCCCTGAA 681  
Db 121 TCAGAAAAAGTGTGCGATCCTGAGATGGCCCAATGAAGATCGACAAATCAAGCCCTGAA 180  
QY 682 GAGAAAACTCTGAGGAAGACAACTGTTGAGATGTTTCACTCATCAGTATCTCTGCT 741  
Db 181 GAGAAAACTCTGAGGAAGACAACTGTTGAGATGTTTCACTCATCAGTATCTCTGCT 240  
QY 742 GCATCTCCATGAATTAAGTCTGATAGACATCAACCGCAAGCACTTTCGCGAGTTC 801  
Db 241 GCATCTCCATGAATTAAGTCTGATAGACATCAACCGCAAGCACTTTCGCGAGTTC 300  
QY 802 TTGCTTTCCGGAAGGAGGATCAGAAATAACAGGGTAAGAAAGGAGTCAAACTCAGAT 861  
Db 301 TTGCTTTCCGGAAGGAGGATCAGAAATAACAGGGTAAGAAAGGAGTCAAACTCAGAT 360  
QY 862 TTGAATGCAAAATCTCTGAAAAAGGTAATGAGCAAGGACCTCAGACTTATCCGATGCAT 921  
Db 361 TTGAATGCAAAATCTCTGAAAAAGGTAATGAGCAAGGACCTCAGACTTATCCGATGCAT 420  
QY 922 ATCCCTGTCTAGTGCATTTGGGAGCTCAATCAAGTCTCTATCAGATCTCTCTTC 980  
Db 421 ATCCCTGTCTAGTGCATTTGGGAGCTCAATCAAGTCTCTATCAGATCTCTCTTC 479

## RESULT 6

US-09-934-455-119  
; Sequence 119, Application US/09934455  
; Publication No. US20030121070A1  
; GENERAL INFORMATION:  
; APPLICANT: Adam, Luc  
; APPLICANT: Creelman, Robert  
; APPLICANT: Dubell, Arnold  
; APPLICANT: Heard, Jacqueline  
; APPLICANT: Jiang, Cai-Zhong  
; APPLICANT: Keddle, James  
; APPLICANT: Pilgrim, Marsha  
; APPLICANT: Ratcliffe, Oliver  
; APPLICANT: Reuber, Lynne  
; APPLICANT: Riechmann, Jose Luis  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Pineda, Omalra  
; TITLE OF INVENTION: Genes for Modifying Plant Traits IV  
; FILE REFERENCE: MBI-0025  
; CURRENT APPLICATION NUMBER: US/09/934,455  
; CURRENT FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227439  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: MBI-0022  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: MBI-0023  
; PRIOR FILING DATE: 2001-04-17

; NUMBER OF SEQ ID NOS: 516  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 119  
; LENGTH: 2526  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; NAME/KEY: CDS  
; LOCATION: (338)..(2275)  
; OTHER INFORMATION: G680  
US-09-934-455-119

Query Match 9.6%; Score 217.2; DB 11; Length 2526;  
Best Local Similarity 49.9%; Pred. No. 1.1e-49;  
Matches 986; Conservative 0; Mismatches 823; Indels 165; Gaps 11;  
QY 235 GTGATGAGACAAATTCCTCTGGAGAAAGATCTGGTTATTATTAAGATCTCGGAAGCCATATACG 294  
Db 335 GTTATGATATAATACTATCTGGAGAAAGATTTATTAGTAAAGGCAAGAACCCATATACA 394  
QY 295 ATACAAAGCAACGTGAAAGGTGACCTGAGGAAGAACATAATAGATTTCATTGAAGCTTTG 354  
Db 395 ATACAAAGCAGCGAGAGCGATGACCTGAGGATGAGCATGAGAGGTTTCTAGAAAGCCCTTG 454  
QY 355 AGGCTTTATGATAGAGCATGGCAGAAAGATTGAAGAACATGTAGCAACAAAAAATGCTGTC 414  
Db 455 AGGCTTTATGGAAGAGCTTGGCAACGAATTTGAAGAACATATTGGGACAAAGACTGCTGTT 514  
QY 415 CAGATAAGAGTCAAGCTCAGAAATTTTCTTCAAGGTAGAGAAAGAGGCTGAAGCTTAA 474  
Db 515 CAGATCAGAAAGTATGCACAAAAGTTCTTCAAAAAGTTGGAGAAAGAGGCTGAAGTTAAA 574  
QY 475 GGTGTAGCTATGGTCAAGCGCTAGACATAGCTATTCTCTCCACGGCTTAAGCGTAAA 534  
Db 575 GGCATCCTGTTGGCAAGCTTTGGACATAGAAATTCGGCTCTCTGCTCTTAAACGAAA 634  
QY 535 CCAAAACAATCCTTATCTCGAAAGACGGGAAGTGAACGATCCTTTATGTCAAAAACCGGT 594  
Db 635 CCCAATACCTCTTATCTCGAAACCTTGGGAACACCGGTACATCTTCTCTCAAGTATCA 694  
QY 595 GTGAATGATGGAAGAGTCCCTTGGATCAGAAAAAGTGTGCGATCTCTGAGATGCCCAAT 654  
Db 695 TCAGCAAAAGATGCAAAAATTTGTTTCATCGGCTCTTCTTCAAGTTGAATCAGCGCTTC 754  
QY 655 GAAGATCGACAAACAATCAAGCCCTGAAGACAAAC-----TCTCAGAA 699  
Db 755 TTGATTTGGAAAAAATGCCGTTCTCTGAAAAACATCAACTGAAAAAGAAAAATCAAGAT 814  
QY 700 GACAACCTGTTTCAAGTTGTTTCACTCATCATGATATCTCTCTGCTGCTCATCTCCATGAATAAA 759  
Db 815 GAGAATTTGCTCGGGTGTCTTCTACTGTGAACAAGTATCCCTTACCACGAAACAGGTAAAT 874  
QY 760 AGTTGTATAGACATCAAAACGCAAGCACTTT-----CGCGAGTTCTTGGCTTC 809  
Db 875 GCGCATTTGAAACAAAGTAAGACCTCAACTGTGCAACACCGGTTCAAGATGTTCCCAAG 934  
QY 810 ACGGGAAGAGGGAAGTCAAGTAACAGGTA-----AGAAAGGAGTCAAC 855  
Db 935 AAGAACAAAGACAAAGATGGTAACGATGGTACTACTGTGACAGCATGCAAAACTACCCCT 994  
QY 856 TCAGATTTGAATGCAAAAATCTCTGGAAAAACCGGTAATGAGCAAGGACCTCAGACTTATCC- 914  
Db 995 TGCGATTTCCACGACATATTGTGAACGGGAATATAGCAAAATGCCCTCAAAATCATCCC 1054  
QY 915 -----G 915  
Db 1055 TCAGGTATGGTATCTCAAGACTTTCATGTTTTCATCTCTATGAGAGAAACTCAGGGCAC 1114  
QY 916 ATGCATATCCCTGTGCTAGTGGCATTGGGGAGCTCAATAACAAGTTCTCTATCACATCCT 975  
Db 1115 GCAATCTTCAAGCTACAAACAGCATCTGCTACTACTACAGTCTCTCATCAAGGTTTCCA 1174  
QY 976 CTTTCAGAGCCAGATAGTATCCCCACACAGTTTGCAGGAGATTATCAGTCTGTTCTCTTAAT 1035



Db 815 GAGAAATGTCGGGTGTTTCTACTGTGAACAAGTATCCCTTACCAACGAAACAGGTAAGT 874  
Qy 760 AGTTGTATAGACATCAACGCAAGCACTTT-----CCGCGAGTTCTTGCGCTTC 809  
Db 875 GCGGACATTTGAACAAGTAAGACCTCACTGTGGACAACCGGGTTCAAGATGTTCCCAAG 934  
Qy 810 ACGGGAAGGGAAGTTCAGATAAACAAGGTA-----AGAAAGGAGTCAAAAC 855  
Db 935 AAGAACAAAGACAAGATGTAACGATGTTACTACTGTGCACAGCATGCAAAACTACCCT 994  
Qy 856 TCAGATTGAATGCAAAATCTCTGGAAGAGGTAAATGAGCAGGACCTCAGACTTATCC- 914  
Db 995 TGGCATTTCCACGACAGATATTGTGAACGGGAATATAGCAAAATGCCCTCAAAATCATCCC 1054  
Qy 915 -----G 915  
Db 1055 TCAGGTATGTTATCAAGACTTCATGTTTTCATCCTATGAGAGAAGAACTACGGGAC 1114  
Qy 916 ATGCATATCCCTGTGCTAGTGCCATTGGGAGCTCAATAACAAGTTCTCTATCACATCCT 975  
Db 1115 GCAAAATCTTCAAGCTACAACAGCATCTGCTACTACTACAGCTTCTCATCAAGCGTTTCCA 1174  
Qy 976 CTTTCAGACCGAGATAGTATCCCCACACAGTTGCGAGGAGATATCAGTCGTTTCTTAAT 1035  
Db 1175 GCTTGTCTATTCACAGGATGATTACCGTTGTTTCTCCAGATATCATCTACTTTTCTCCAAT 1234  
Qy 1036 CATATAATGTCAAACCCCTTTTCAAAACACCGGCTCTTTATACTGCCCAACTTTTCGGCTCA 1095  
Db 1235 CTTATTATGTCAACTCTCTCAGAAATCTGCGAGCTCATGCTGCGAGCTACATCTCGTGT 1294  
Qy 1096 TCATTTTGGCCCTCCCG-----ATTCTAGTGGTGGCTCACCTGTTCCAGGGAAC 1143  
Db 1295 TCGGTCTGGCCTTATGCGAGTGTGCGGAATCTCGTGAATTCATCAACCCCAATGAGCTCT 1354  
Qy 1144 TCACCTCCGAATCTGGCTGCCATGGCCGAGCAGCACTGTTGCGAGCTGCTAGTGTGGTG 1203  
Db 1355 TCTCTCCAAGTATACTGCCATGCGCTGTCTACAGTAGCTGCTGCAACTGCTGGTG 1414  
Qy 1204 GCTGCCAATGGATTATTAACCTTTATGTGCTCTCTTAGTTTCAGGTGTTTCACTAGTCAT 1263  
Db 1415 GCTTCTCATGGACTTCTCTGTATGCGTCTCAGCTCCATACATGTTGTTCCATTTCTCA 1474  
Qy 1264 CTCCATCTACTTTTGGACATCATGTGATGATGATGATGATGATGATGATGATGATGATG 1323  
Db 1475 ACTGTTGCAAGTTTCCAACTCCAGCAATGACTGAAATGGAATACCGTTGAAATACTCAAC 1534  
Qy 1324 CATGGTCTGTGAGAGCCGAGAGCAAGCAACTCCGAGGCATCAAGGCTCGATCTTCA 1383  
Db 1535 TTTGAGAAAACAAACACAGCTCTGCAAGATCAAACTTGGCTTCGAAATCTCCAGCTTCA 1594  
Qy 1384 CTGGACTCAGAGGATGTTGAAAAT-----AAGAGTAAACCACTGTTGTCATGAGCAG 1434  
Db 1595 TCATCTGATGATTACATGAGACTGGAGTAACCAAGCTAAATGCCACTCAAAACCAAT 1654  
Qy 1435 CTTCTGCAACCTGAGAGTGAATGCAA-----AGGTTTCAGATGAGGACGAGA 1482  
Db 1655 GATGATAAAATTCAGAGAGGTTGTTGTTACTGCGCTGTGCATGACTCAAAACACTGCCCA 1714  
Qy 1483 GACAGAAACAAGTTGACCGGCTCTGCTGCTCAAACTCCGCTGAGTAGTATGAT 1542  
Db 1715 AAGAAAAATCTTTGGGACCGCTCATCTGTGTGGCTCAAAATACACCTTCAGGAGTAGCGCA 1774  
Qy 1543 GTTAGGCGGATGCATCAAGAAAGGCAAGAGGATGGCAACCAATGGTGGAGTGAAGAAACG 1602  
Db 1775 GAACTGATGCATTAGATAAATGGAAGAAAGATTAAGAGGATGTGAGGAGACAGATGAG 1834  
Qy 1603 AAT-----GAAGACACTAATAAACCCTCAAACTTCAGAGTCCAAATGACCGCGCAGTAGA 1656  
Db 1835 AATCAGCCAGATGTTATTGAGTTAAATAACCGTAAAGATTAAATGAGAGCAACAACAGC 1894  
Qy 1657 ATCAGCTCCAATATAACCGATCCATGGAAGTCTGTGCTGACGAGGTTGAAATGCGCTTC 1716

Db 1895 AACAAATGCAACTACTGATTCGTGGAAGGAAGTCTCCGAGAGGGTCTGTATAGCGTTT 1954  
Qy 1717 CAAGCTCTCTTCCAGAGAGGTATTGCGCGCAAGTTTTCATCATTCGAGAGACACAGA 1776  
Db 1955 CAGGCTCTCTTTGCAAGAGAAAGATTGCTCTCAAAGCTTTTCGCTCTCTCAAGTGGCAGAG 2014  
Qy 1777 GAGGAAGAACAAACAACAAGATATCCAAATGGCACTTGATCTTAACTTCCACA 1836  
Db 2015 AATGTGAATAGAAAACAAAGTGACACGT-----CAATGCCATTTGGCTCTTAATTTCAA 2068  
Qy 1837 GCTCAGTTAAACACAGTTGATGATCAAGAGGAGAGAAACACAGAGATTTCTTGAATC 1896  
Db 2069 AGCCAGGATTCTTGTCTGCAGACCAAGA-----AGGAGTAGTAATGATC 2113  
Qy 1897 GATTAGATGCTTCAAGCTAATGCTAGAGGAAGAACAGGTTTAAACCATACAAAGA 1956  
Db 2114 GGTGTTGGAACATGCAAGAGTCTTAAACGAGACAGAGGATTTAAGCCATACAAGA 2173  
Qy 1957 TGTTCATGGAAGCCAAAGAAAGTAGAATCCTCAACAACAATCCTATCATTTATGTGAA 2016  
Db 2174 TGTTCATGGAAGTGAAGAGAGAGCAAGTTGGGAACATAAA-----CAATCAAAGTAT 2227  
Qy 2017 CAGAAAGATCCCAACCGGATGCGGTTGGAAACTCAAGCTTCCACATGAGACTCT 2070  
Db 2228 GAAAAGTCTGCAAAAGGCTTCGATTGGAAGGAGAGAGCTTCTACATGACAGACT 2281

## RESULT 8

US-09-938-842A-1116  
; Sequence 1116, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; TITLE OF INVENTION: SAME, AND METHODS OF USE  
; FILE REFERENCE: SCRIPI300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 1116  
; LENGTH: 1938  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-1116

Query Match 9.4%; Score 213; DB 10; Length 1938;  
Best Local Similarity 49.9%; Pred. No. 1.4e-48;  
Matches 980; Conservative 0; Mismatches 820; Indels 165; Gaps 11;

Qy 238 ATGGAGACAAATTCGTCTCGAGAAGATCTGGTTATTAAAGACTCGGAAGCCATATACGATA 297  
Db 1 ATGGGATCTAATACATCTCGAGAAGAAATTTATTAGCTAAGCAAGAAAGCCATATACAATA 60  
Qy 298 ACAAGACACGTAAGGTTGAGTGGAGTGAAGAACATGATGAGCAACAAACCTGCTGTCAG 357  
Db 61 ACAAGACGAGAGCGATGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 120  
Qy 358 CTTTATGTTAGAGCTGGCAGAGATTGAAGAACATGATGAGCAACAAACCTGCTGTCAG 417  
Db 121 CTTTATGGAAGAGCTTGGCAACGAAATTGAAGAACATATTGGGACAAAGACTGCTGTTTCA 180  
Qy 418 ATAAGAGTACGCTCAGAAATTTTCTCAGAGGTAGAGAAAGAGGCTGAAGCTAAAGGT 477  
Db 181 ATCAGAAGTCTATGCACAAAGTTCTTCAAAAGTTGGAGAAAGAGGCTGAAGTTAAAGGC 240





```
; APPLICANT: Adam, Luc
; APPLICANT: Broun, Pierre
; APPLICANT: Pineda, Onaira
; APPLICANT: Reuber, Lynne
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Keddie, James
; APPLICANT: Zhang, James
; APPLICANT: Benito, Maria-Ines
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fromm, Mike
; TITLE OF INVENTION: PLANT GENE SEQUENCES I
; FILE REFERENCE: MBI-0003
; CURRENT APPLICATION NUMBER: US/10/295,403
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/394,519
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 60/101,349
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/103,312
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/108,734
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/113,409
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 1237
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (73)..(951)
; OTHER INFORMATION: G673
US-10-295-403-49

Query Match          3.7%; Score 83; DB 14; Length 1237;
Best Local Similarity 60.4%; Pred. No. 4e-12;
Matches 137; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 237 GATGGAGACAAATTCGTCTCGAGAGATCTGGTTATTAACTCGGAAGCCATACGAT 296
Db 144 GATTGCAACACCGGAGCTGGTGAACACCGGAGAGAGAGTGGAGAACTTATACAAT 203
QY 297 AACAAAGCAACGTGAAGGTGGAGTCTGAGGAGAACATATAGATTTCATTGAAGCTTTGAG 356
Db 204 CACCAAGTCTAGAGAGAGTTGGACTGAAGGAGAACACGACAGTTTCTGGAAGCTCTTCA 263
QY 357 GCTTTATGTAGACATGCGCAGAGATTGAAGAACATGTAGCAACAAAACACTGCTGTCCA 416
Db 264 ATTGTTGTGCTGAGTGGAGAAAGATAGAAAGATTTTGTGGTTCAAGACAGTTATTCA 323
QY 417 GATAAGAAGTCACGCTCAGAAATTTTCTCCAAGGTAGAGAAAGAGG 463
Db 324 GATCAGAGGACCATGCCCAAAATACTTCTAAAGGTCCAAAAAATG 370

RESULT 13
US-09-878-574-707
; Sequence 707, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 1575

; SEQ ID NO 707
; LENGTH: 365
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LfB3028-047-Q1-B1-E4
US-09-878-574-707

Query Match          3.3%; Score 74.8; DB 10; Length 365;
Best Local Similarity 65.7%; Pred. No. 3.3e-10;
Matches 109; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 274 AAGACTCGGAAGCCATATACGATAACAAACGACGTAAGAGGTGGACTGAGGAAGAACAT 333
Db 198 AAGTAAGAAACCTTAGACCATACCAAGTCCAGGGAGAGTTGGACTGAGGAAGACAC 257
QY 334 AATGATTTCATTGAAGCTTTGAGGCTTTATGTTAGACCATGGCAGAGATTGAAGAACAT 393
Db 258 GACAAGTTTCTCGAAGCTCTTCAATTATTGACAGGGGACTGGAAGAAAATTGAAGATTTT 317
QY 394 GTAGCAACAAAACTGCTGCCAGATAAGAAAGTCACGCTCAGAAAT 439
Db 318 GTAGGTTCAAAAAACAGTTATTCAAGTTTCAAGCCATGCTCAGAAAT 363

RESULT 14
US-09-814-353-4739
; Sequence 4739, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4739
; LENGTH: 664
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 55, 54, 159, 161, 174, 177, 178, 180, 182, 185, 212, 215,
; LOCATION: 216, 219, 220, 226, 237, 247, 248, 265, 269, 278, 281, 283,
; LOCATION: 289, 294, 298, 299, 300, 301, 302, 304, 305, 307, 308, 316,
; LOCATION: 327, 333, 334, 335, 336, 339, 343, 344, 345, 348, 368
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 377, 383, 386, 388, 390, 409, 429, 431, 433, 439, 447, 450,
; LOCATION: 452, 460, 462, 473, 474, 475, 477, 484, 486, 508, 509, 510,
; LOCATION: 511, 513, 514, 515, 518, 519, 520, 522, 525, 528, 530, 532,
; LOCATION: 533, 541, 542, 543, 544, 547, 550, 552, 561, 564, 570
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 573, 575, 578, 584, 600, 601, 603, 606, 607, 616, 623, 625,
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; LOCATION: 626, 642
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-4739

Query Match      2.4%; Score 55.2; DB 12; Length 664;
Best Local Similarity 52.4%; Pred. No. 0.00017;
Matches 108; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 2049 TCAAGCTTCCACATGAGACTCTATTTTCATCTGATCTGTGTGTTGACTCTGTTTTTAAG 2108
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6 TCGAGCGCGCGCCGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 65

QY 2109 TTTTCAAGCACTGCTACATTTCTTTTCTTTTTCAGGCTTTGTATTTGTTTCTCTGT 2168
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 66 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 125

QY 2169 CCATAGTCTTCTGTAAACATTTTGACTCTCTATTTATTCACAAATCATAACTGTTTAATC 2228
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 126 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 185

QY 2229 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2254
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 186 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 211

RESULT 15
US-09-814-353-11036
; Sequence 11036, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-008B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11036
; LENGTH: 664
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 53, 54, 159, 161, 174, 177, 178, 180, 182, 185, 212, 215,
; LOCATION: 216, 219, 220, 226, 237, 247, 248, 265, 269, 278, 281, 283,
; LOCATION: 289, 294, 298, 300, 301, 302, 304, 305, 307, 308, 316,
; LOCATION: 327, 333, 334, 335, 336, 339, 343, 344, 345, 348, 368
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 377, 383, 386, 388, 390, 409, 429, 431, 433, 439, 447, 450,
; LOCATION: 452, 460, 462, 473, 474, 475, 477, 484, 486, 508, 509, 510,
; LOCATION: 511, 513, 514, 515, 518, 519, 520, 522, 525, 528, 530, 532,
; LOCATION: 533, 541, 542, 543, 544, 547, 550, 552, 561, 564, 570
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 573, 575, 578, 584, 600, 601, 603, 606, 607, 616, 623, 625,
; LOCATION: 626, 642
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-11036

Query Match      2.4%; Score 55.2; DB 12; Length 664;
Best Local Similarity 52.4%; Pred. No. 0.00017;
Matches 108; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 2049 TCAAGCTTCCACATGAGACTCTATTTTCATCTGATCTGTGTGTTGACTCTGTTTTTAAG 2108
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6 TCGAGCGCGCGCCGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 65

QY 2109 TTTTCAAGCACTGCTACATTTCTTTTCTTTTTCAGGCTTTGTATTTGTTTCTCTGT 2168
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 66 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 125

QY 2169 CCATAGTCTTCTGTAAACATTTTGACTCTCTATTTATTCACAAATCATAACTGTTTAATC 2228
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 126 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 185

QY 2229 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2254
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 186 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 211

Search completed: November 24, 2003, 18:59:29
Job time : 668.933 secs
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